PANEL A

PANEL B

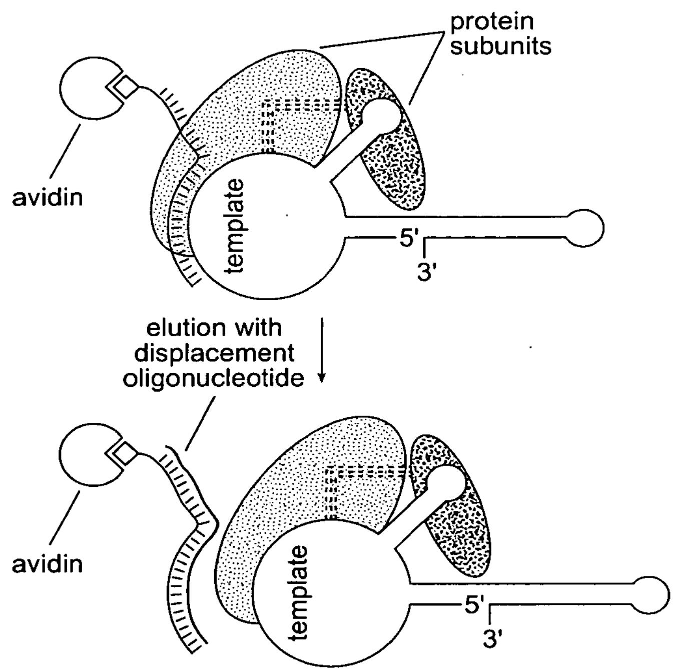


FIG. 1

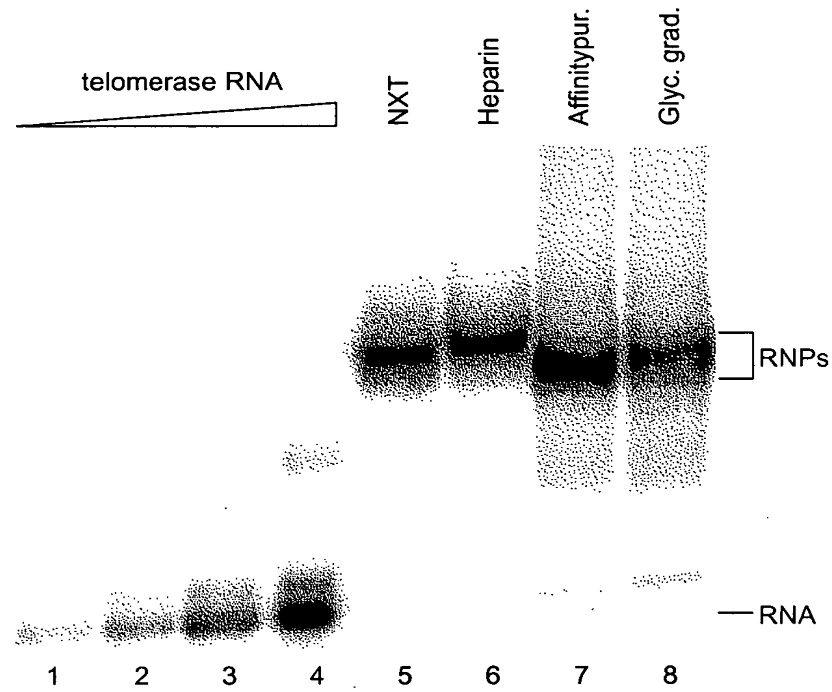

telomerase RNA
NXT
Heparin
Affinitypur.
Glyc. grad.
RNPs
RNA
1
2
3
4
5
6
7
8

FIG. 2

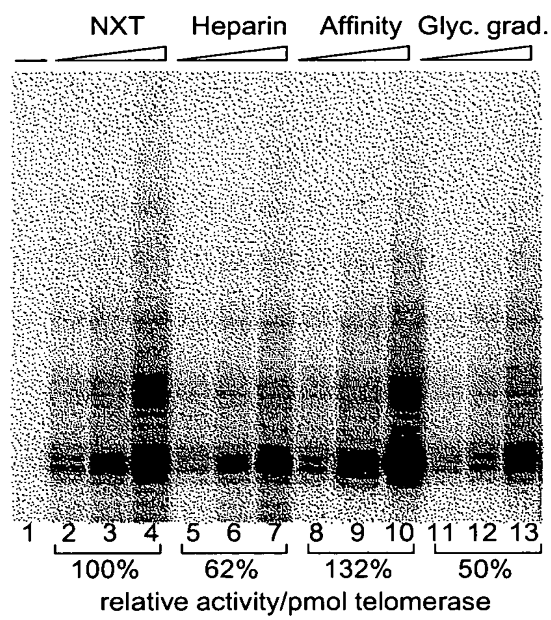

NXT
Heparin
Affinity
Glyc. grad.
1 2 3 4 5 6 7 8 9 10 11 12 13
100%
62%
132%
50%
relative activity/pmol telomerase

FIG. 3

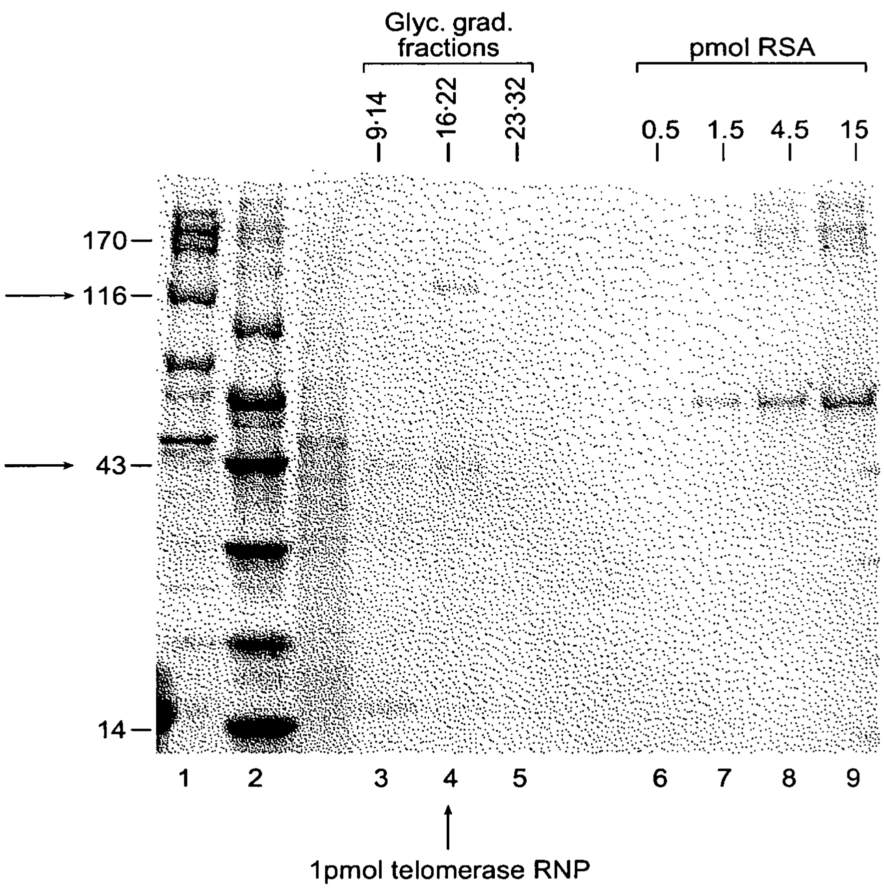
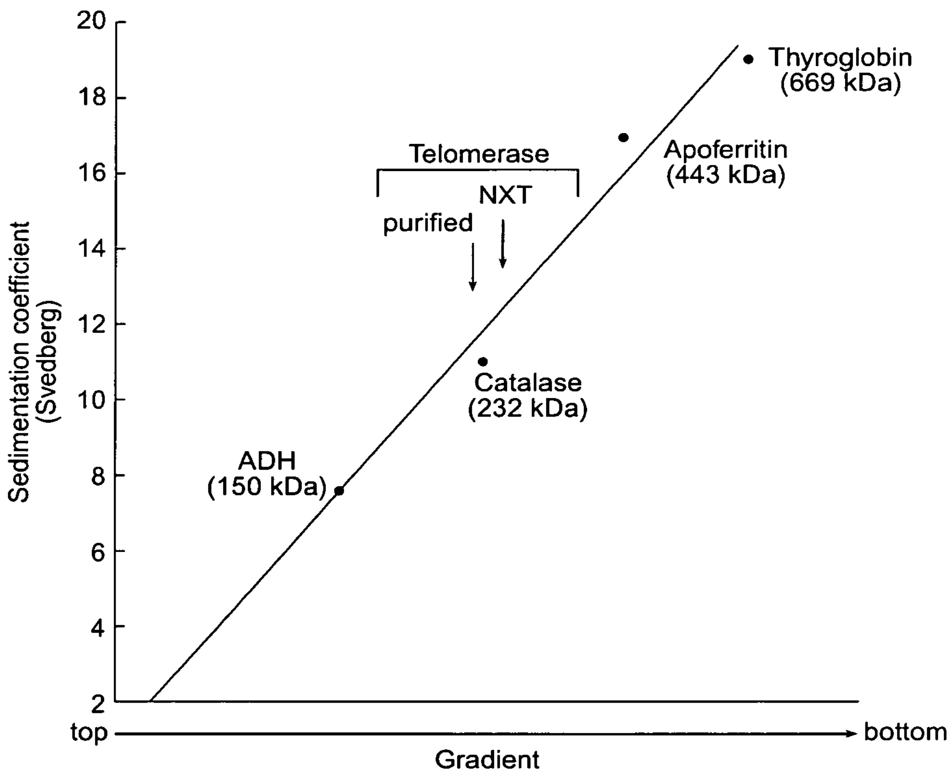

Glyc. grad.
fractions
pmol RSA
9·14
16·22
23·32
0.5
1.5
4.5
15
170
116
43
14
1
2
3
4
5
6
7
8
9
1pmol telomerase RNP

FIG. 4



20
18
16
14
12
10
8
6
4
2
Sedimentation coefficient (Svedberg)
Thyroglobin (669 kDa)
Apoferritin (443 kDa)
Telomerase
NXT
purified
Catalase (232 kDa)
ADH (150 kDa)
top
bottom
Gradient

FIG. 5

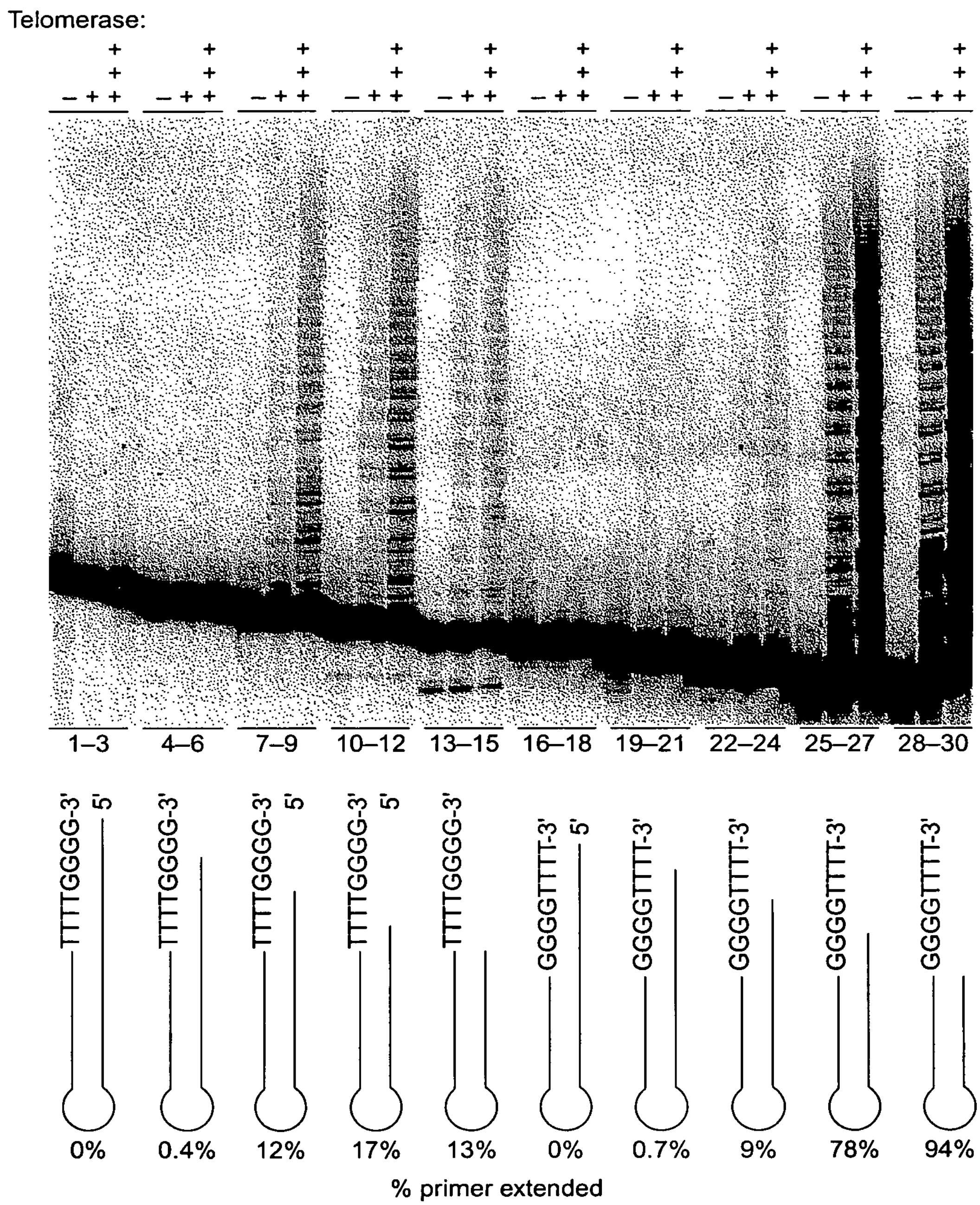

Telomerase:
– + +
1–3
4–6
7–9
10–12
13–15
16–18
19–21
22–24
25–27
28–30
TTTTGGGG-3'
5'
GGGGTTTT-3'
0%
0.4%
12%
17%
13%
0%
0.7%
9%
78%
94%
% primer extended

FIG. 6

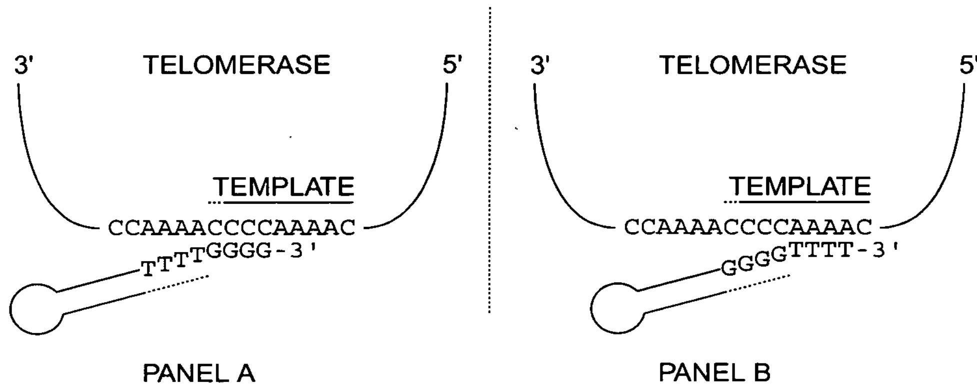


FIG. 7

```
   1  CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
  51  GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101  TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151  GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201  TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251  CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301  AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351  AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401  TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
 451  CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501  GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551  AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
 601  TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651  TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
 701  AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751  CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801  TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851  TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901  TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951  AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001  TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051  AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101  AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151  CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201  GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251  TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301  GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351  AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401  AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451  ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501  GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551  CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601  ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651  AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701  AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751  GGGGTTTTGG GG
```

FIG. 11

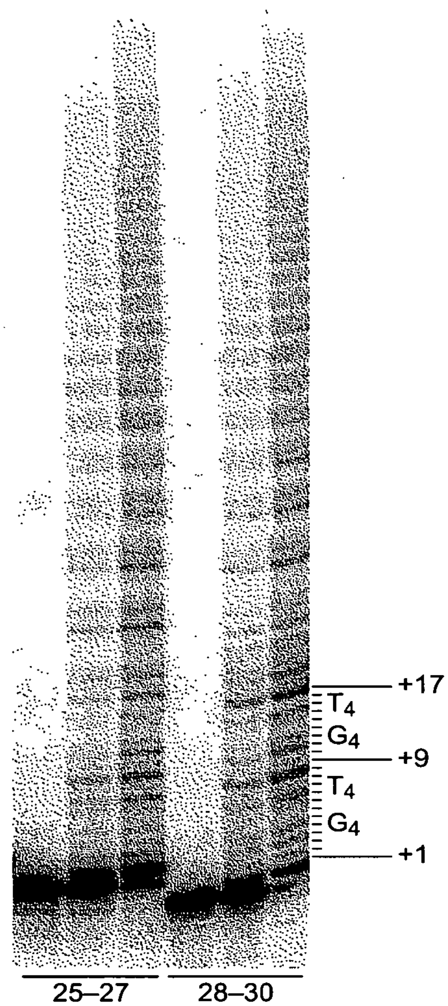


FIG. 8

```
   1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
  51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC
1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT
2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
```

FIG. 9

2401	CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC
2451	TTTTGATTAC	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAAACTT
2501	ATAAACGTAA	GTCGTGAAAA	TGGATTTAAA	TTCAATATGA	AGAAACTACA
2551	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	TGCAAAATAC	GGAATGGATA
2601	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	GATTGGCATC
2651	TCAATTGATA	TGAAAACTCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT
2701	AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT
2751	CAATGTGGCT	CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC
2801	CATTATTTTA	GAAAGACGAT	TACAACCGAA	GACTTTGCGA	ATAAAACTCT
2851	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	ATACATGCAA	TGAGCCAAAG
2901	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	TATGATCGAC
2951	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA
3001	CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG
3051	ACTTTTTCCT	TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA
3101	AAGTACATTT	TCAACAGAGT	TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA
3151	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	TCAATATGAT	GCATAGTCGA
3201	CTATTCTAAC	TTATTTTGGA	AAGTTAATTT	TCAATTTTTG	TCTTATATAC
3251	TGGGGTTTTG	GGGTTTTGGG	GTTTTGGGG		

FIG. 9
(CONTINUED)

1	MEVDVDNQAD	NHGIHSALKT	CEEIKEAKTL	YSWIQKVIRC	RNQSQSHYKD
51	LEDIKIFAQT	NIVATPRDYN	EEDFKVIARK	EVFSTGLMIE	LIDKCLVELL
101	SSSDVSDRQK	LQCFGFQLKG	NQLAKTHLLT	ALSTQKQYFF	QDEWNQVRAM
151	IGNELFRHLY	TKYLIFQRTS	EGTLVQFCGN	NVFDHLKVND	KFDKKQKGGA
201	ADMNEPRCCS	TCKYNVKNEK	DHFLNNINVP	NWNNMKSRTR	IFYCTHFNRN
251	NQFFKKHEFV	SNKNNISAMD	RAQTIFTNIF	RFNRIRKKLK	DKVIEKIAYM
301	LEKVKDFNFN	YYLTKSCPLP	ENWRERKQKI	ENLINKTREE	KSKYYEELFS
351	YTTDNKCVTQ	FINEFFYNIL	PKDFLTGRNR	KNFQKKVKKY	VELNKHELIH
401	KNLLLEKINT	REISWMQVET	SAKHFYYFDH	ENIYVLWKLL	RWIFEDLVVS
451	LIRCFFYVTE	QQKSYSKTYY	YRKNIWDVIM	KMSIADLKKE	TLAEVQEKEV
501	EEWKKSLGFA	PGKLRLIPKK	TTFRPIMTFN	KKIVNSDRKT	TKLTTNTKLL
551	NSHLMLKTLK	NRMFKDPFGF	AVFNYDDVMK	KYEEFVCKWK	QVGQPKLFFA
601	TMDIEKCYDS	VNREKLSTFL	KTTKLLSSDF	WIMTAQILKR	KNNIVIDSKN
651	FRKKEMKDYF	RQKFQKIALE	GGQYPTLFSV	LENEQNDLNA	KKTLIVEAKQ
701	RNYFKKDNLL	QPVINICQYN	YINFNGKFYK	QTKGIPQGLC	VSSILSSFYY
751	ATLEESSLGF	LRDESMNPEN	PNVNLLMRLT	DDYLLITTQE	NNAVLFIEKL
801	INVSRENGFK	FNMKKLQTSF	PLSPSKFAKY	GMDSVEEQNI	VQDYCDWIGI
851	SIDMKTLALM	PNINLRIEGI	LCTLNLNMQT	KKASMWLKKK	LKSFLMNNIT
901	HYFRKTITTE	DFANKTLNKL	FISGGYKYMQ	CAKEYKDHFK	KNLAMSSMID
951	LEVSKIIYSV	TRAFFKYLVC	NIKDTIFGEE	HYPDFFLSTL	KHFIEIFSTK
1001	KYIFNRVCMI	LKAKEAKLKS	DQCQSLIQYD	A	

FIG. 10

```
     CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAAGAAAAAATTGAGGTAGTTTAGA
   1 ---------+---------+---------+---------+---------+---------+ 60
     GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTAACTCCATCAAATCT

a    P  Q  N  P  K  T  P  K  P  L  *  K  K  K  K  L  R  *  F  R   -
b     P  K  T  P  K  P  Q  N  P  Y  K  K  R  K  N  *  G  S  L  E  -
c      P  K  P  Q  N  P  K  T  P  I  K  K  E  K  I  E  V  V  *  K -

     AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
  61 ---------+---------+---------+---------+---------+---------+ 120
     TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a    N  K  I  L  F  P  H  K  W  R  W  I  L  I  W  M  I  *  K  I   -
b     I  K  Y  Y  S  R  T  N  G  D  G  Y  *  F  G  *  Y  R  K  F  -
c      *  N  I  I  P  A  Q  M  E  M  D  I  D  L  D  D  I  E  N  L -

     TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 ---------+---------+---------+---------+---------+---------+ 180
     ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a    Y  F  L  I  H  S  T  S  I  A  A  L  V  V  T  R  K  D  A  K   -
b     T  S  *  Y  I  Q  Q  V  *  Q  L  L  *  *  Q  E  R  M  Q  N  -
c      L  P  N  T  F  N  K  Y  S  S  S  C  S  D  K  K  G  C  K  T -

     CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 ---------+---------+---------+---------+---------+---------+ 240
     GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

a    H  *  N  L  A  R  N  R  L  H  *  L  F  Q  S  C  K  N  N  *   -
b     I  E  I  W  L  E  I  A  F  I  D  Y  S  K  V  A  K  T  I  R  -
c      L  K  S  G  S  K  S  P  S  L  T  I  P  K  L  Q  K  Q  L  E -

     AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
 241 ---------+---------+---------+---------+---------+---------+ 300
     TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a    S  S  T  S  R  M  Q  I  F  I  T  I  L  S  *  E  N  *  F  *   -
b     V  L  L  L  G  C  K  S  L  *  R  F  F  L  E  K  I  S  F  K  -
c      F  Y  F  S  D  A  N  L  Y  N  D  S  F  L  R  K  L  V  L  K -

     AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 ---------+---------+---------+---------+---------+---------+ 360
     TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a    K  A  E  S  K  E  *  K  L  K  H  Y  *  C  L  N  K  I  R  *   -
b     K  R  R  A  K  S  R  N  *  N  I  T  N  V  *  I  K  S  G  N  -
c      S  G  E  Q  R  V  E  I  E  T  L  L  M  F  K  *  N  Q  V  M -

     TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 ---------+---------+---------+---------+---------+---------+ 420
     ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a    *  G  L  F  Y  F  L  D  H  F  L  R  S  I  M  E  K  I  T  *   -
b     E  D  Y  S  I  F  *  I  T  S  *  G  A  L  W  R  K  L  L  N  -
c      R  I  I  L  F  F  R  S  L  L  K  E  H  Y  G  E  N  Y  L  I -
```

FIG. 12

```
    TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
421 ---------+---------+---------+---------+---------+---------+ 480
    ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

a   Y  *  K  V  N  S  L  D  Y  F  P  S  Q  Q  *  *  V  Y  *  I  -
b    T  K  R  *  T  V  W  I  I  S  L  A  N  N  D  E  Y  I  K  F  -
c     L  K  G  K  Q  F  G  L  F  P  *  P  T  M  M  S  I  L  N  S -

    CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481 ---------+---------+---------+---------+---------+---------+ 540
    GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a   H  M  R  M  S  Q  R  I  S  I  H  Q  T  Y  Q  R  Q  T  R  Y  -
b    I  *  E  *  V  K  G  S  R  Y  I  R  L  T  K  D  K  L  A  I  -
c     Y  E  N  E  S  K  D  L  D  T  S  D  L  P  K  T  N  S  L  * -

    AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
541 ---------+---------+---------+---------+---------+---------+ 600
    TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC

a   K  T  Q  E  K  V  *  *  S  N  S  R  R  T  Y  C  I  Y  Y  S  -
b    K  R  K  K  K  F  D  N  R  T  A  E  E  L  I  A  F  T  I  R  -
c     N  A  R  K  S  L  I  I  E  Q  Q  K  N  L  L  H  L  L  F  V -

    TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT
601 ---------+---------+---------+---------+---------+---------+ 660
    ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a   Y  G  F  Y  Y  N  C  F  R  Y  R  R  *  T  P  E  S  *  D  N  -
b    M  G  F  I  T  I  V  L  G  I  D  G  E  L  P  S  L  E  T  I  -
c     W  V  L  L  Q  L  F  *  V  S  T  V  N  S  R  V  L  R  Q  L -

    TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
661 ---------+---------+---------+---------+---------+---------+ 720
    ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a   *  K  S  C  L  Q  L  K  E  S  Q  F  *  K  F  *  C  V  C  H  -
b    E  K  A  V  Y  N  *  R  N  R  S  S  E  S  S  D  V  Y  A  I  -
c     K  K  L  F  T  T  E  G  I  A  V  L  K  V  L  M  C  M  P  L -

    TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 ---------+---------+---------+---------+---------+---------+ 780
    ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a   Y  F  V  N  *  S  Q  I  S  Y  L  N  L  M  D  S  Y  R  N  K  -
b    I  L  *  I  N  L  K  Y  L  I  S  I  *  W  I  A  I  E  T  N  -
c     F  C  E  L  I  S  N  I  L  S  Q  F  N  G  *  L  *  K  Q  T -

    CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
781 ---------+---------+---------+---------+---------+---------+ 840
    GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a   P  N  K  P  C  K  F  N  G  I  Y  V  K  S  F  G  T  N  A  H  -
b    Q  I  N  H  A  S  L  M  E  Y  T  L  N  P  L  G  Q  M  H  T  -
c     K  *  T  M  Q  V  *  W  N  I  R  *  I  L  W  D  K  C  T  L -

    TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841 ---------+---------+---------+---------+---------+---------+ 900
    ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a   *  I  Y  I  G  F  L  K  H  R  Y  T  E  C  F  R  D  *  F  S  -
b    E  F  I  L  D  S  *  S  I  D  T  Q  N  A  L  E  T  D  L  A  -
c     N  L  Y  W  I  L  K  A  *  I  H  R  M  L  *  R  L  I  *  L -
```

FIG. 12
(CONTINUED)

```
     TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
 901 ---------+---------+---------+---------+---------+---------+ 960
     AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a    L  Q  Q  I  T  C  F  D  Y  S  C  S  S  L  I  S  L  K  E  A  -
b     Y  N  R  L  P  V  L  I  T  L  A  H  L  L  Y  L  *  K  K  Q  -
c      T  T  D  Y  L  F  *  L  L  L  L  I  S  Y  I  F  K  R  S  R -

     GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
 961 ---------+---------+---------+---------+---------+---------+ 1020
     CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG

a    G  E  M  K  R  R  L  K  K  E  I  S  K  F  V  D  S  S  V  T  -
b     A  K  *  K  E  D  *  R  K  R  F  Q  N  L  L  I  L  L  *  P  -
c      R  N  E  K  K  T  K  E  R  D  F  K  I  C  *  F  F  C  N  R -

     GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC
1021 ---------+---------+---------+---------+---------+---------+ 1080
     CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG

a    G  I  N  N  K  N  I  S  N  E  K  E  E  E  L  S  Q  S  *  F  -
b     E  L  T  T  R  I  L  A  T  K  K  K  K  S  Y  H  N  P  D  S  -
c      N  *  Q  Q  E  Y  *  Q  R  K  R  R  R  A  I  T  I  L  I  L -

     TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081 ---------+---------+---------+---------+---------+---------+ 1140
     AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a    L  K  I  S  K  I  P  G  K  R  D  T  F  I  K  I  H  I  L  *  -
b     *  R  F  Q  K  F  Q  V  R  E  I  H  S  L  K  F  I  Y  Y  S  -
c      K  D  F  K  N  S  R  *  E  R  Y  I  H  *  N  S  Y  I  I  V -

     TTTTTCATTTCACAGCTGTTATTTCTTTTATCTTAACAATATTTTTGATTAGCTGGAA
1141 ---------+---------+---------+---------+---------+---------+ 1200
     AAAAAGTAAAGTGTCGACAATAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT

a    F  F  I  S  Q  L  L  F  S  F  I  L  T  I  F  F  D  *  L  E  -
b     F  S  F  H  S  C  Y  F  L  L  S  *  Q  Y  F  L  I  S  W  K  -
c      F  H  F  T  A  V  I  F  F  Y  L  N  N  I  F  *  L  A  G  S -

     GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
1201 ---------+---------+---------+---------+---------+---------+ 1260
     CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a    V  K  S  I  K  *  E  K  R  *  T  E  V  T  *  L  I  H  I  H  -
b     *  K  V  S  N  K  R  S  A  R  L  R  *  L  S  L  F  T  F  I  -
c      K  K  Y  Q  I  R  E  A  L  D  *  G  N  L  A  Y  S  H  S  * -

     AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT

a    R  S  T  F  I  Y  P  I  R  *  *  G  N  S  S  H  P  F  *  K  -
b     D  R  P  S  Y  I  Q  Y  D  D  K  E  T  A  V  I  R  F  K  N  -
c      I  D  L  H  I  S  N  T  M  I  R  K  Q  Q  S  S  V  L  K  I -

     TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a    *  C  Y  E  D  *  I  F  R  V  K  K  W  S  R  N  L  N  Q  K  -
b     S  A  M  R  T  K  F  L  E  S  R  N  G  A  E  I  L  I  K  K  -
c      V  L  *  G  L  N  F  *  S  Q  E  M  E  P  K  S  *  S  K  R -
```

FIG. 12
(CONTINUED)

```
        GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
   1381 ---------+---------+---------+---------+---------+---------+ 1440
        CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

   a    E  L  R  R  Y  C  K  R  I  E  L  *  I  F  R  *  *  V  L  P  -
   b     N  C  V  D  I  A  K  E  S  N  S  K  S  F  V  N  K  Y  Y  Q  -
   c      I  A  S  I  L  Q  K  N  R  T  L  N  L  S  L  I  S  I  T  N -

        ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
   1441 ---------+---------+---------+---------+---------+---------+ 1500
        TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

   a    I  L  I  D  C  R  D  *  R  G  N  C  T  E  D  H  *  R  N  K  -
   b     S  *  L  I  E  E  I  D  E  A  T  A  Q  K  I  I  K  E  I  K  -
   c      L  D  *  L  K  R  L  T  R  Q  L  H  R  R  S  L  K  K  *  S -

        GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
   1501 ---------+---------+---------+---------+---------+---------+ 1560
        CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

   a    V  T  F  I  N  *  R  I  N  *  I  T  N  I  E  I  S  D  L  Q  -
   b     *  L  L  L  I  R  E  *  T  K  L  L  I  *  R  S  A  I  F  N  -
   c      N  F  Y  *  L  E  N  K  L  N  Y  *  Y  R  D  Q  R  S  S  I -

        TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
   1561 ---------+---------+---------+---------+---------+---------+ 1620
        AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA

   a    L  T  K  *  K  L  N  *  S  *  T  I  K  N  T  N  L  G  Q  N  -
   b     *  R  N  K  S  *  T  K  V  R  Q  *  K  I  Q  T  L  V  K  I  -
   c      D  E  I  K  A  E  L  K  L  D  N  K  K  Y  K  P  W  S  K  Y -

        ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
   1621 ---------+---------+---------+---------+---------+---------+ 1680
        TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

   a    I  E  E  G  K  E  D  Q  L  A  K  E  K  I  R  Q  *  I  K  *  -
   b     L  R  K  E  K  K  T  S  *  Q  K  K  K  *  G  N  K  *  N  E  -
   c      *  G  R  K  R  R  P  V  S  K  R  K  N  K  A  I  N  K  M  S -

        GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTCAATAATTTATTGAAAAGAGGGGTT
   1681 ---------+---------+---------+---------+---------+---------+ 1740
        CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAGTTATTAAATAACTTTTCTCCCCAA

   a    V  Q  K  *  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V  -
   b     Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  *  K  E  G  F  -
   c      T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F -

        TTGGGGTTTTGGGGTTTTGGGG
   1741 ---------+---------+-- 1762
        AACCCCAAAACCCCAAAACCCC

   a    L  G  F  W  G  F  G     -
   b     W  G  F  G  V  L  G    -
   c      G  V  L  G  F  W      -
```

FIG. 12
(CONTINUED)

```
  2 EVDVQNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL  51
    |:::  | :.::|:  :|    |.::|      ::. .  |  |..|.|.|
 19 ELELEMQENQNDIQVRVK....IDDPKQY..LVNVTAACLLQEGSYYQDK  62

 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100
    ::      ..::    : .|.|  ..|.. .|: ..:| |  ...::|.:
 63 DERRYIITKALL....EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107

101 SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
                 ..: ....: ...: .|:  ..:.:   |:.||  :
108 .............CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144

151 IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA 200
    ::.. | :||             | .: :.:: ..|.... :::  ::
145 FDATEFKNLY.............LDRILSQDIRKELTFRKCLQRCVRSKF 181

201 ADMNE...PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF 247
    .::||   .::|..:  . |... ::|. .| ..|:. |.:
182 SEFNEYQLGKYCTES..QRKKTMFRYLSVTNKQKWDQTKKK......... 220

248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI 297
     |.: ...| :. .:.:: | .: :     :|:.:   | ||. |:.||
221 .RKENLLTKLQAIKESEDKSKRETG.....DIMNVEDAIKALKPAVMKKI 264

298 AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE 347
    | . . :|                     :. | ..: |.| |.|   :.:
265 AKRQNAMK..... ...............KHMKAPKIPNSTLESKYLTFKD 294

348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE 397
    |:..   ...      .| .|.||.|.: .. :  .  .   .  ..:| .|
295 LIKFCHISEP.....KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE 338

398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL 447
    |  |..:|  .|:| .: . :..|. :  :  .| ...  :||.: :
339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN.. 386

448 VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
                                |:| ::.|
387 .............................ILKAGVSD........... 394

498 KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT 547
                                                ||:.
395 ..........................................TTHS 398

548 KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
        |                                :|. |.|:..|:
399 IVINK..............................ICEPKAVENSKM 415

598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID 647
    |   :. .. :.|| | :.. :|..|    .:    :.:||   |:  |::
416 F..PLQFFSAIEAVN.EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE 457

648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE 697
    ..:  ||:|           .||..: ..:..| |. ..:. .. .| :.
458 KTDEEKKDM...........ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496

698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
      .. :.. .    :::.  .   .   :    |.  ::. .| .. :|:
497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL 546

748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI 797
    :  .  |.||: ::...| ..:.. ::: :
547 MVKQRCEKSSFYIFSSPSSQCNKCYLEVDL.................... 576
```

FIG. 13

```
798  EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
                       .:::::: .|.| ||.. .|::: ..:. ::::| .  ....|
577  .......PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617

847  WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
     |.|   ||.. .  .:||:| .:|: .:                ||.|. :
618  NIVILSDMMIAEGYSDINVRGSSIVNSI..............KKYKDEVN 653

897  NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM 945
      ||. :    .:. |:::                  |::. :.|:.: :: | ::|
654  PNIKIF...AVDLEGYG.............KCLNLGDEFNENNYIKIFGM 687

946  SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
     |. |               :|:: ... :.                  :::|
688  SDSI..............LKFISAKQGGA................NMVE 706

996  IFSTKKYIFNRVC 1008
     ::   |.: :.::.
707  VI..KNFALQKIG 717
```

FIG. 13
(CONTINUED)

```
132  LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFQRTSE..GTLVQFC 178
     :| ..|         ....| |||| :   :. .. ::..  |   |  | .
  1  MSRRNQ.......KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI  43

179  GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN  228
      :: :. ||..:. :. ..|...| :|              | .|..::|..:|
 44  KEEDLKLLKFKNQDQDGNSGNDDDDEE.........NNSNKQQELLRRVN  84

229  VPNWNNMKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN  278
                     ::... |::||  |:.| : .   ..:.  .|
 85  .................QIKQQVQLIKK...VGSKVEKDLNLNEDENKKN  114

279  IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ  328
      :. ..::..   ...|. .    : | ::::.. |..|.. . ::|| .
115  GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY  164

329  KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG  377
     ..|.::: .:::|                  .:|. : |:   |   : ||::.
165  DTEKWFEISHDQK.............NYVSIYANQKTSYCWWLKDYFNK  200

378  RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY  427
     .| .::. .:.:.   .. |:.  : : :.|.  : |:  |:..
201  NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID......  242

428  FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI  475
     .: :| ..:: |||:: :| : :  ||: :  | .| .:.|.  . ..|
243  VNFDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI  290

476  WDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP  525
     :.|:. .         .:|: .::  ..:.: ... . |. |..
291  FAVVFSHR..........HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ  330

526  IMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY  575
     :  |...:  |  |.|: .  |:|.. .|. :... :. . . || |.
331  VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL  378
```

FIG. 14

```
576  DDVMKKYEEFVCKWKQVGQPKLF. . ....FATMDIEKCYDS..VNREK  615
     : .:||       :. |  |. |          :. :.:| ..:.  :.::|
379  NVLLKKVKH  ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK  426

516  LSTFL......KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK  657
     |...|      |. |:|   |:.  ||   ||. :   ... ||:::... .
427  LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ  476

558  DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKTLIVEAKQRNYFK  705
     .  .  .      |:      |  |     | :|:...    ::|.|  |
477  EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN....LQATQEIY..  520

706  KDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE  755
       | |    |           .|        :.  :  ...|     |.||:
521  .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.....YETLNN  564

756  SSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR  305
           |:  | | .||: |     ||:          .:..::  ||.
565  .....LKRCSVNISNPHGNISYELTN.........KDSTFYKFKLTLNQE  500


806  ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK  855
          |:.:|  |..|.:.  | ||.: .|:|. : ::..|..|: : ::.
601  LQHAKYTFK..QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ  648

856  TLALMPNINLRIEGILCTLNLNMQT..KKASMWLKK..KLKSFLMNNITH  901
     .:.:         | ::|:. |:....  |.. :::|.  .||.:    .|.
649  NVNI.......IASLLYPNNIQKNPFNKPNLLFFKQFEQLKNLENVSINC  691

902  YFRKTI...TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM  948
     .: . |       | :....  | ||    | .:|:  :|.. ||.  .:..:
692  ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL  741

949  IDLEVSKIIYSVT.............RAFFKYLVCNIKDT..IFGEEHY  982
      :: ... :    |                 :||:. |.  ||:.  .:.  .:
742  NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF  791

983  PDFFLS  TLKHFIEIFSTKKY IFNRVCMILKAKEAKLKSDQCQSLIQ  1028
     .:   :|     .|    | :|..||   . |:      ...   | ..::.|.|:.
792  DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK  840
```

FIG. 14
(CONTINUED)

```
  4  DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK......   47
     ::.  ..||.   :.::...| |..  :||.|....  :|| .|.
617  NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP  666

 48  ......LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLM   86
          : ||:| .  .  .|:  :::|   :|.| .: :|      |..:::
667  FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL  716
```

FIG. 15

```
  1  MEMDIDLDDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS...   42
      |: |. .   .||       ...|.. |:| |...:. . | || ..:
491  IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC  540

 43  .LTIPKLQKQ......LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL   85
      |.:  : ||       : :: |... :|.::| .: |.::| |..::.||
541  ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL  589
```

FIG. 16

```
telomerase p43   LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La         ICHQUEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA      ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La    ILRQVEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p      CLKQVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT
```

FIG. 18

```
   1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
  61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
 481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aactttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccccac tttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a
```

FIG. 19

```
                       Motif A                          Motif B

Consensus            h--hDh---h--h                    h---+-QG---SP
telomerase p123     GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL
Dong (LINE)         KNRNLHCTYDDYKKAFDSIPHSWLIQVLEIYKIN- 28-RQIAIKKGIYQGDSLSPLWFCLALNPLSHQLHNDR
a1 S.c. (groupII)   FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPRVCVQGAPTSPALCNAVLLRLDRRLAGLA
HIV-RT              LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-  7-GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQN
L8543.12            VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK

                     Motif C                          Motif D          Motif E

Consensus           h--YhDDhhh                        Gh-h---K          h-hLGh-h
telomerase p123     -14-LMRLTDDYLLITTQENN-0-AVLFIEKLINVSRENGFKFNMKKLQT-23-QDYCDWIGISI
Dong (LINE)         -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KCLYKYLGFQQ
a1 S.c. (groupII)   -55-YVRYADDILIGVLGSKN-2-KIIKRDLNNFLNS.LGLTINEEKTLI- 4-ETPARFLGYNI
HIV-RT              - 4-IYQYMDDLYVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDKKHQK- 0-EPPFLWMGYEL
L8543.12            - 8-ILKLADDFLIISTDQQQ.......VINIKKLAMGGFQKYNAKANR-41-IRSKSSKGIFR
```

FIG. 17

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLA
VYIRNELYIRTTTNYIVAFCVVHKNTQPFIEKYFNKAVLLPNDL
LEVCEFAQVLYIFDATEFKNLYLDRILSQDIRKELTFRKCLQRC
VRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTKKK
RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI
AKRQNAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
YKILGKKYPKTEEEYKAAFGDSASAPFNPELAGKRMKIEISKTW
ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
KQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGA
KKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL
EVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHV
DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
VEVIKNFALQKIGQK

FIG. 20

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK
EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQ
QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITEE
QVKYQNLVFNMDYQLDLNESGGHRRHRRETDYDTEKWFEISHDQ
KNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAEFY
AFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERF
NILNIRSSYTRNQYNFEKIGELLETIFAVVFSHRHLQGIHLQVP
CEAFQYLVNSSSQISVKDSQLQVYSFSTDLKLVDTNKVQDYFKF
LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSIP
TQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNL
KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLLI
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCSVNI
SNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFN
NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPN
NIQKNPFNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEF
LEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPELNQVYINQ
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFD
QNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQ
ELLKACDEKGVLVKAYYKFPLCLPTGTYYDYNSDRW

FIG. 22

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKI
ARNEDVNNSLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLI
NYTVIQFNGQFFTQIVGNRCNEPHLPPKWVQRSSSSSATAAQIK
QLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLREA
IFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPL
EGTVLDLSHLSRQSPKERVLKFIIVILQKLLPQEMFGSKKNKGK
IIKNLNLLLSLPLNGYLPFDSLLKKLRLKDFRWLFISDIWFTKH
NFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTIVYFR
HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRI
IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEY
LRNKRPTSFTKIYSPTQIADRIKEFKQRLLKKFNNVLPELYFMK
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
LWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDK
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNNFHIRSKS
SKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE
YEVRFTILNGFLESLSSNTSKFKDNIILLRKEIQHLQAYIYIYI
HIVN

FIG. 23

1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa
121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt
781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga
901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatcaaaa aatcttaaat ttttaagatt
1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac
1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1501 aactccaagc gaaagcacaa gtggtatgaa atttttttgat catctttctg aattaaccga
1561 gcttgaagat ttcagcgtta acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttctttatg aactgacaaa
1801 taaagattct acttttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc
1921 ttcctcatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
2041 tcctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 cctttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatatttta gttatttaat tcattatttt aagtaaataa ttatttttca atcatttttt
2821 aaaaaatcg

FIG. 21

```
Oxytricha          LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Euplotes           LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT
```

FIG. 24

```
ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT
AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC
```

FIG. 26

```
                                                            Motif 0
human                                AKFLHWLMSVYVVELLRSFFYVTETTFQKNR
tez1       ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR
EST2       LKDFRWLFISD---IWFTKHNFENLNQLAIFCISWLFRQLIPKIIQTFFYCTEISSTVT-
p123       TREISWMQVET-SAKHFYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
                                            . *.     .   ....*** **

                                                              Motif 1
human      LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1       TVYFRKDIWKLLCRPFI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
EST2       IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNNEF
p123       TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKK--TTF
             ..*.  *  .     *    *                               .* .**

           Motif 2
human      RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1       RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF
EST2       RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123       RPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKY
           * *                *                *                     .  .

                          Motif 3 (A)
tez1       KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2       KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123       EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
             . *          .*   *   *** . .      .*   *
```

FIG. 25

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 27

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGC
CAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC
TGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGA
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT
CAACTACGAGCGGGCGCG

FIG. 28

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLVSTF
PNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWL
VLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCR
PFITSMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTN
QTLRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM
FRIVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRIAD

FIG. 29

```
ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga
actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta
ccaagtataaggacaaaaagaacaacttccttcccccctaaagactttactttattaatttacttttcaaatatatttcg
ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat
agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc
ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag
gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttttgatgcttgcacacgtctagcatg
attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctattttctattctcatgttgtt
ccaaatatgtatcatctcgtattaggctttttttccgttttactcctggaatcgtaccttttttcactattccccctaatga
ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa
gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc
actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTACCTTAAATGATT
ATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAACGCTTGAGAAGCGATGTACAAACG
TCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGTAAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAA
ATGCTCACAGTCAGAGgtatatatattttttgttttgatttttttctattcgggatagctaatatatgggcagCTAATAGC
GAATGTTGTAAAACAGATGTTCGATGAAAGTTTTGAGCGTCGAAGGAATCTACTGATGAAAGGGTTTTCCATGgtaaggt
attctaattgtgaaatatttacctgcaattactgtttcaaagagattgtatttaaccgataaagAATCATGAAGATTTTC
GAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTACCTTATATCTATACTTGAGTCAAAA
AATTGGCAACTTTTGTTAGAAATgtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatagTATCGG
CAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTCCAAATGACAATTACCTTCAGATTTCTG
GCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGTCAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACT
CAAAATAAAAGCGCCCGCAAAGAAGTTTCCTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTA
TAAGAAGTTTAAGCAAGgtaactaatactgttatccttcataactaattttagATCTATATTTTAACTTACACTCTATTT
GTGATCGGAACACAGTACACATGTGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAG
CAATTGCACAAAGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA
ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGACACCCACGATG
ATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATCCATTCTTGTTCGAGTGTTTCCT
AAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGgtattgtataaaatttattaccactaacgatttt
accagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTACATTATTTAATGAGTAACATAAAGgtaa
tatgccaaatttttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGTCCTTGGAAAAAGGTCAAATGCG
AAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGGAATTCATCTACTGGCTATACAATTCGTTTATAAT
ACCTATTTTACAATCTTTTTTTTATATCACTGAATCAAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTT
GGAAACTCTTGTGCCGACCCTTTATTACATCAATGAAAATGGAAGCGTTTGAAAAAATAAACGAGgtattttaaagtatt
ttttgcaaaaagctaatattttcagAACAATGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTC
TATTACCTAAGAAGAATACCTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaatttttggtcat
caatgtactttacttctaatctattattagcagATGGGTTCAAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACG
ACCTGTGGCATCGATACTGAAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGC
```

FIG. 30

TTCTTACTTTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGgtaattatataatgcgcgattcctcattattaatttt
gcagGCGTAAGAAGTATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATT
GTTAAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCGAGCTACAAA
AAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagtttatttttttcattggaatttttttaacaaattctttttttagTTGAT
ATGGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGTGGATTATTG
GACCAAAAGTTCTTCTGAAATTTTTAAAATGCTCAAGGAACATCTCTCTGGACACATTGTTAAGgtataccaattgttga
attgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTCAGGGCTCAATTCTGT
CATCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTTTACGAAAAAGAAAGGATCAGTGTTG
TTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAAAGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGg
tgagttgctgtcattcctaagttctaaccgttgaagGATTTGAGAAACACAATTTTTCTACGAGCCTGGAGAAAACAGTA
ATAAACTTTGAAAATAGTAATGGGATAATAAACAATACTTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTT
CTCTGTGAACATGAGGTCTCTTGATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAG
AGCTGACGAAACATATGGGGAAATCTTTTTTTTACAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaata
atcagATCGAGCCTTGCATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATAT
ATATAGGCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCCAAAGAA
TGTTCATAACGGgtgagtacttatttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAA
AATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAAATGgtacgtgt
cggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTTTCAAA
TATCATCCATGCTTCGAACAGCTAATATACCAATTTCAGTCATTGACTGATCTTATCAAGCCGCTAAGACCAGTTTTGCG
ACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcattttcaatttattatatacatcctttattactggtgtc
ttaaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctc
gttattagttttgattgacttgtctttatccttatactttttaagaaagattgacagtggttgctgactactgcccacatg
cccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttt
tctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttctaaacaagggggattaagcatatccgaagg
aaaagagagtaatatacccagtgttgttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaatt
ttggtgaccgaattttggtaaaagccccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggat
agtttgaatactaatagctcatttaatgtcttatataaggttttgtttttttcctgacttcaattttgcatgggtgaaaag
aaatagtgttaagccattattggattccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattg
aagcttatgaggcttcaaaaactcctcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagct
gctgaggagaagcctaatttttttgcaaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtat
ctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctcta
cgcagttaagtgaccaaaggtacc

FIG. 30
(CONTINUED)

```
EST2 pep              FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN    40
Euplotes pep          FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE    43
Trans of tetrahymen   ------KHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ    44

Consensus             FFY.TE..K. .S..YYYRK. IW...-KL.. ...---F..K .......V..    50

EST2 pep              NVCRNHNSY- ---------- TLSNFNHSKM RIIPKKSNNE FRIIAIPCRG    79
Euplotes pep          KEVEEWKKSL ---------- ---GFAPGKG RLIPKKTT-- FRPIMTFNKK    78
Trans of tetrahymen   KIQLEEENLE KVEEKLIPED SFQKYPQGKL RIIPKKGS-- FRPIMTFLRK    92

Consensus             K...E..... ---------- ....F..GKL RIIPKK..-- FRPIMTF.RK   100

EST2 pep              ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE   129
Euplotes pep          IVNSDRKTTK LTTNTKLLNS HLMLKTLKN- ------RMFK -DPFGFAVFN   120
Trans of tetrahymen   DKQKNIK--- LNLNQILMDS QLVFRNLKD- ------ML-G -QKIGYSVFD   130

Consensus             ......K..K LN.N..L..S QL.L..LKN- ------.... -..IG..VF.   150

EST2 pep              FKQRLLKKFN NVL------- -PELYFMKFD VKSCYD                   157
Euplotes pep          YD-DVMKKYE EFVCKWKQVH CPKLFFATMD IEKCYD                   155
Trans of tetrahymen   NK-QISEKFA QFIEKWKNKG RPCLYYVTL- ------                   158

Consensus             .K-...KKF. .F..KWK..G .P.LYF.T.D ...CYD                   186
```

FIG. 31

```
S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE


A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV
```

FIG. 32

```
        Poly 4
                   t       t       c
            t a    a   g   c   c   t c g
        5'- cag acc aaa gga att cca taa gg -3'
            Q   T   K   G   I   P   Q   G

                        4(B')


            5(c')

     D   D   Y   L   L   I   T
 3'- ctg ctg atg gag gag tag tgg -5'
       a   a   a a a a a   a   a
                   t   t   t   t
                           c   c
                          Poly 1
```

FIG. 34

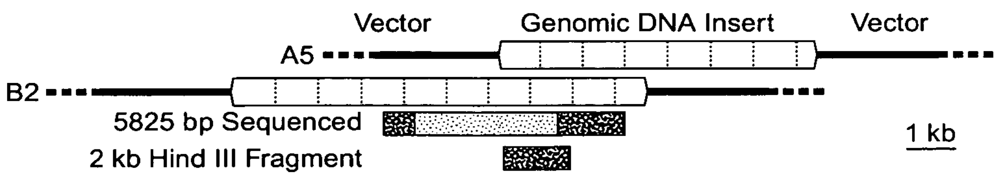


FIG. 33A

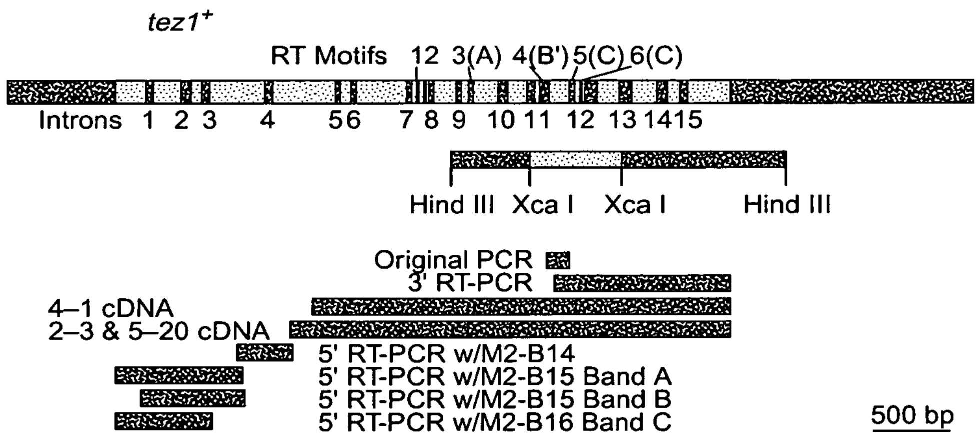


FIG. 33B

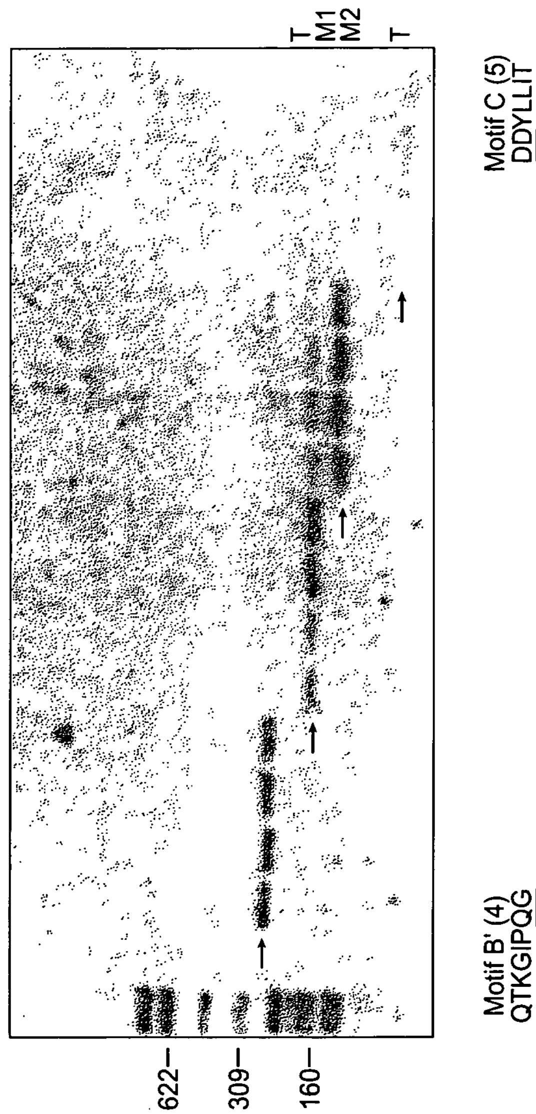


FIG. 35

```
Ot                 LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123      KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2              SILSSFLCHFYMEDLIDEYLSFTKKK--------GSVLLRVV
Sc_p103      DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS------QDTLILKLADDFLIIS
                    .*   .        * .    *               .....

Q   K   V   G   I   P   Q   G
caa aaa gtt ggt atc cct cag gg......    <---Actual Genomic Sequence.

Poly 4
      t       t       c
t a   a   g   c   c   t c g
cag acc aaa gga att cca taa gg ---->

 ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

        K   G   I   P   S   G   S   I   L   S   S   F   L   C   H   F   Y   M
```

FIG. 36

```
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E   D   L   I   D   E   Y   L   S   F   T   K   K   K   G   S   V   L   L   R


GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V   V   D   D   Y   L   L   I   T

  <---- ctg ctg atg gag gag tag tgg
          a   a   a a a a a   a   a
                    t   t     t   t
                              c   c
                             Poly 1

   .....gac gat ttc ctc ttt ata aca......  <---Actual Genomic Sequence
        D   D   F   L   F   I   T
```

FIG. 36
(CONTINUED)

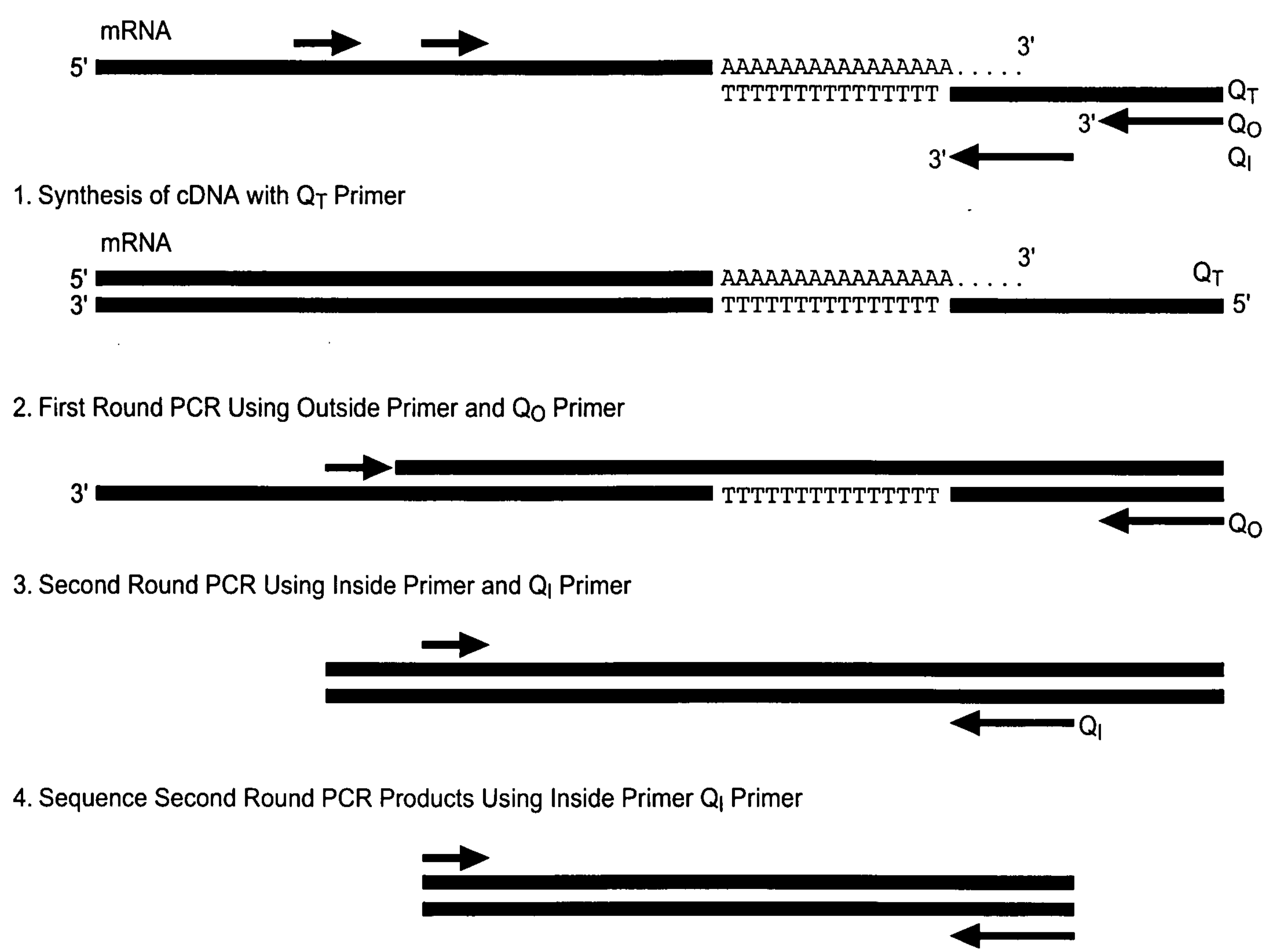

mRNA
5'
AAAAAAAAAAAAAAAA.....
3'
TTTTTTTTTTTTTTT
Q_T
3'
Q_O
3'
Q_I
1. Synthesis of cDNA with Q_T Primer
mRNA
5'
3'
AAAAAAAAAAAAAAAA.....
3'
TTTTTTTTTTTTTTT
Q_T
5'
2. First Round PCR Using Outside Primer and Q_O Primer
3'
TTTTTTTTTTTTTTT
Q_O
3. Second Round PCR Using Inside Primer and Q_I Primer
Q_I
4. Sequence Second Round PCR Products Using Inside Primer Q_I Primer

FIG. 37

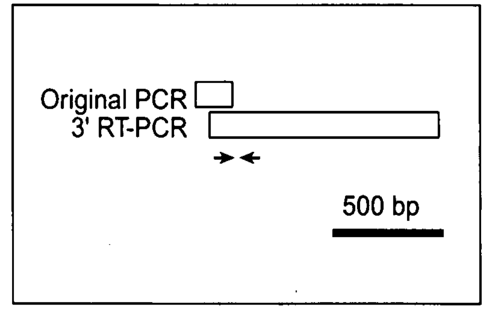
A. Genomic Libraries

Size Selected Libraries from P. Nurese
- 3~4 kb
- 5~7 kb
- 7~8 kb
- 11~12 kb

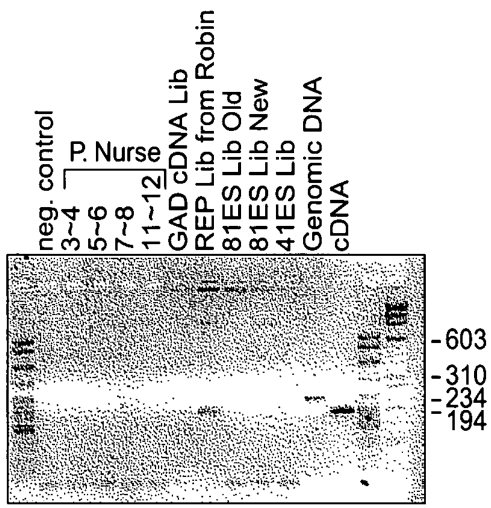
Libraries from J.A. Wise
- Sau 3a Partial Digest
- Hind III Partial Digest

cDNA Libraries
- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B.



C.



D.

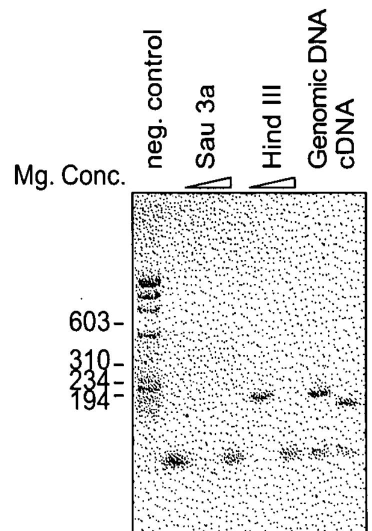


FIG. 38

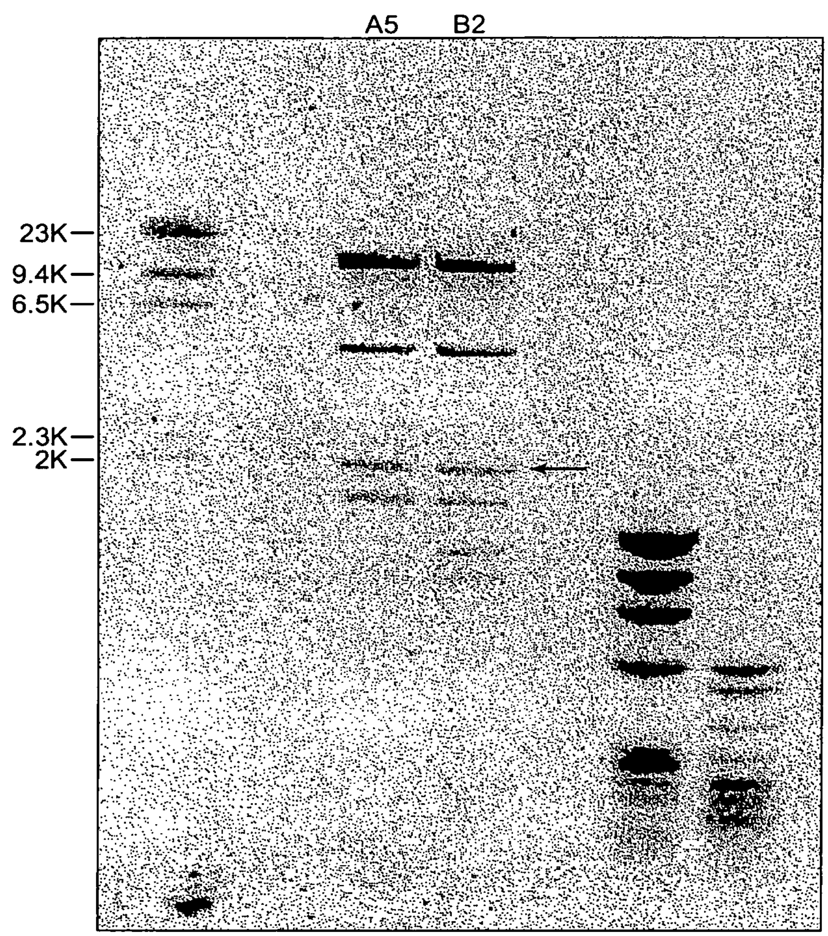


FIG. 39

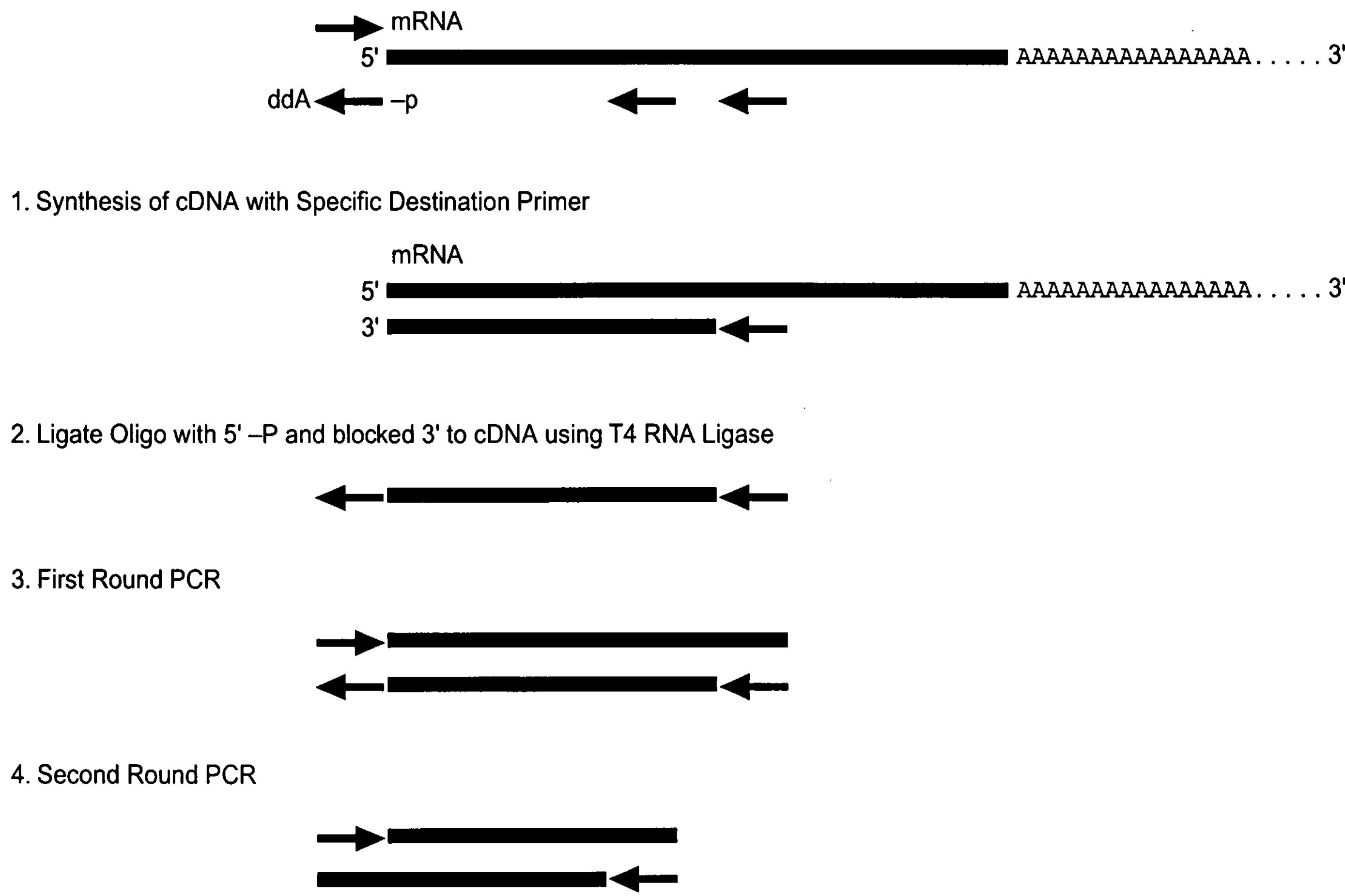

mRNA
5'
AAAAAAAAAAAAAAAA. . . . . 3'
ddA
–p
1. Synthesis of cDNA with Specific Destination Primer
mRNA
5'
AAAAAAAAAAAAAAAA. . . . . 3'
3'
2. Ligate Oligo with 5' –P and blocked 3' to cDNA using T4 RNA Ligase
3. First Round PCR
4. Second Round PCR

FIG. 40

```
                                Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
E.a. p123  (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
                  *           *** **         * *    *

             Motif 1    Motif 2     K
            p hh h K     hR h       R
S.p. Tez1p  AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.c. Est2p  SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
E.a. p123   GKLRLIPKK--TTFRPIMTFNKKIV ...(61)...
              *  ***    ** *

            Motif 3(A) AF
                h  hDh  GY  h
S.p. Tez1p  KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.c. Est2p  ELYFMKFDVKSCYDSIPRMECMRILK ...(75)...
E.a. p123   KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
              *   *   ***           *

             Motif 4(B')
                  hPQG   pP hh    h
S.p. Tez1p  YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.c. Est2p  YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123   YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
           *    *  **   *          *      *

                Y Motif 5(C)                Motif 6(D)
             h  F DDhhh                     Gh h  cK  h
S.p. Tez1p  VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS .(205)
S.c. Est2p  LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
E.a. p123   LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLS .(209)
                 ** *  *                             *       *
```

FIG. 41

A.

```
Sp_Tip1p    1  ----------MTEHHTPKSRILRFLENQYVYLCT  24
Sc_Est2p    1  ---------------------------MKILFEF   7
Ea_p123     1  MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW   33

Sp_Tip1p   25  LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS  57
Sc_Est2p    8  IQDKLDIDLQTN--STYK---ENLKCGHFNGLD  35
Ea_p123    34  IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN  61

Sp_Tip1p   58  IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN  90
Sc_Est2p   36  EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH  67
Ea_p123    62  IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK  94

Sp_Tip1p   91  VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH 122
Sc_Est2p   68  CIIYLLTGELYN---NVLTFGYKIARNED----  93
Ea_p123    95  CLVELLSSSDVSDRQKLQCFGFQLKGNQ----- 122

Sp_Tip1p  123  VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG 155
Sc_Est2p   94  ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG 123
Ea_p123   123  ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG 152

Sp_Tip1p  156  SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN 188
Sc_Est2p  124  TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123   153  NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH 185

Sp_Tip1p  189  NVFEETVSKKRKRTIETSITQN---KSARKEVS 218
Sc_Est2p  156  HLPPKWVQ--RSSSSSATAAQI---KQLTEPVT 183
Ea_p123   186  LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK 217
```

FIG. 42

A.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 42

(CONTINUED)

A.

```
Sp_Tip1p  426  EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY  458
Sc_Est2p  363  CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY  394
Ea_p123   438  KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY  470

Sp_Tip1p  459  FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD  491
Sc_Est2p  395  FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS  427
Ea_p123   471  YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW  503

Sp_Tip1p  492  TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL  522
Sc_Est2p  428  YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD  460
Ea_p123   504  KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV  534

Sp_Tip1p  523  IKMGSNKKMLVSTNQTLRPVASILKHLINE---  552
Sc_Est2p  461  EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT  491
Ea_p123   535  NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF  564

Sp_Tip1p  553  ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK  584
Sc_Est2p  492  SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL  524
Ea_p123   565  KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL  597

Sp_Tip1p  585  YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F  616
Sc_Est2p  525  YFMKFDVKSCYDSIPRMECMRILKDALKNENGF  557
Ea_p123   598  FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF  630

Sp_Tip1p  617  VIRKYATIHATSDRATKN---------------  634
Sc_Est2p  558  FVRSQYFFNTNTG--------------------  570
Ea_p123   631  WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK  663
```

FIG. 42
(CONTINUED)

A.

```
Sp_Tip1p  635  F V S E A F S Y F D M V P F E K V V Q L L S - - M K T S D T L F V  665
Sc_Est2p  571  - - - - - - - - - - - V L K L F N V V N A S R - - V P K P Y E L Y I  591
Ea_p123   664  F Q K I A L E G G Q Y P T L F S V L E N E Q N D L N A K K T L I V  696

Sp_Tip1p  666  D F V D Y W T K S S S E I F K M L K E H L S G H I V K I G N S Q Y  698
Sc_Est2p  592  D N V R T V H L S N Q D V I N V V E M E I F K T A L W V E D K C Y  624
Ea_p123   697  E A K Q R N Y F K K D N L L Q P V I N I C Q Y N Y I N F N G K F Y  729

Sp_Tip1p  699  L Q K V G I P Q G S I L S S F L C H F Y M E D L I D E Y L S F T K  731
Sc_Est2p  625  I R E D G L F Q G S S L S A P I V D L V Y D D L L E F Y S E F K A  657
Ea_p123   730  K Q T K G I P Q G L C V S S I L S S F Y Y A T L E E S S L G F L R  762

Sp_Tip1p  732  K K G - - - - - - - - - S V L L R V V D D F L F I T V N K K D A K K  756
Sc_Est2p  658  S P S Q D - - - - - - - T L I L K L A D D F L I I S T D Q Q Q V I N  684
Ea_p123   763  D E S M N P E N P N V N L L M R L T D D Y L L I T T Q E N N A V L  795

Sp_Tip1p  757  F L N L S L R G F E K H N F S T S L E K T V I N F E N S N G - - -  786
Sc_Est2p  685  I K K L A M G G F Q K Y N A K A N R D K I L A V S S Q S D - - - -  713
Ea_p123   796  F I E K L I N V S R E N G F K F N M K K L Q T S F P L S P S K F A  828

Sp_Tip1p  787  - - - I I N N T F F N E S K K R M P F F G F S V N M R S L D T L L  816
Sc_Est2p  714  - - - - D D T V I Q F C A - - - M H I F V K E L E V W K H S S T M  739
Ea_p123   829  K Y G M D S V E E Q N I V Q D Y C D W I G I S I D M K T L A L M P  861

Sp_Tip1p  817  A C P K I D E A L F N S T S V E L T K H M G K S F F Y K I L R S S  849
Sc_Est2p  740  N N F H I R S K S S K G I F R S L I A L F N T R I S Y K T I D T N  772
Ea_p123   862  N I N L R I E G I L C T L N L N M Q T K K A S M W L K K K L K S F  894
```

FIG. 42
(CONTINUED)

A.

```
Sp_Tip1p  850   LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR  882
Sc_Est2p  773   LNSTNTVLMQIDHVVKNISEC------------  793
Ea_p123   895   LMNNITHYFRKTITTEDFANKTLNKLFISGGYK  927

Sp_Tip1p  883   AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK  915
Sc_Est2p  794   ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM  821
Ea_p123   928   YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV  960

Sp_Tip1p  916   LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS  948
Sc_Est2p  822   TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN  854
Ea_p123   961   TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF  993

Sp_Tip1p  949   FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF  981
Sc_Est2p  855   TS----------KFKDNIILLRKEIQHLQAYIY  877
Ea_p123   994   IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC  1023

Sp_Tip1p  982   LHRRIAD-                           988
Sc_Est2p  878   IYIHIVN-                           884
Ea_p123   1024  QSLIQYDA                           1031
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p    1   ----------MTEHHTPKSRILRFLENQYVVYLCT   24
Sc_Est2p    1   ----------------------------MKILFEF    7
Ea_p123     1   MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW     33

Sp_Tip1p   25   LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS     57
Sc_Est2p    8   IQDKLDIDLQTN--STYK---ENLKCGHFNGLD     35
Ea_p123    34   IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN     61

Sp_Tip1p   58   IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN     90
Sc_Est2p   36   EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH     67
Ea_p123    62   IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK     94

Sp_Tip1p   91   VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH    122
Sc_Est2p   68   CIIYLLTGELYN---NVLTFGYKIARNED----     93
Ea_p123    95   CLVELLSSSDVSDRQKLQCFGFQLKGNQ-----    122

Sp_Tip1p  123   VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG    155
Sc_Est2p   94   ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG    123
Ea_p123   123   ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG    152

Sp_Tip1p  156   SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN    188
Sc_Est2p  124   TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP    155
Ea_p123   153   NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH    185

Sp_Tip1p  189   NVFEETVSKKRKRTIETSITQN---KSARKEVS    218
Sc_Est2p  156   HLPPKWVQ--RSSSSSATAAQI---KQLTEPVT    183
Ea_p123   186   LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK    217
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p  426  E F I Y W L Y N S F I I P I L Q S F F Y I T E S S D L R N R T V Y  458
Sc_Est2p  363  C F I S W L F R Q L I P K I I Q T F F Y C T E I S S T V T - I V Y  394
Ea_p123   438  K L L R W I F E D L V V S L I R C F F Y V T E Q Q K S Y S K T Y Y  470

Sp_Tip1p  459  F R K D I W K L L C R P F I T S M K M E A F E K I N E N N V R M D  491
Sc_Est2p  395  F R H D T W N K L I T P F I V E Y F K T Y L V E N N V C R N H N S  427
Ea_p123   471  Y R K N I W D V I M K M S I A D L K K E T L A E V Q E K E V E E W  503

Sp_Tip1p  492  T Q K T T L P P A V I R L L P K K - - N T F R L I T N L R K R F L  522
Sc_Est2p  428  Y T L S N F N H S K M R I I P K K S N N E F R I I A I P C R G A D  460
Ea_p123   504  K K S L G F A P G K L R L I P K K - - T T F R P I M T F N K K I V  534

Sp_Tip1p  523  I K M G S N K K M L V S T N Q T L R P V A S I L K H L I N E - - -  552
Sc_Est2p  461  E E E - - F T I Y K E N H K N A I Q P T Q K I L E Y L R N K R P T  491
Ea_p123   535  N S D - - R K T T K L T T N T K L L N S H L M L K T L K N R - M F  564

Sp_Tip1p  553  E S S G I P F N L E V Y M K L L T F K K D L L K H R M F G R - K K  584
Sc_Est2p  492  S F T K I Y S P T Q I A D R I K E F K Q R L L K K F N N V L P E L  524
Ea_p123   565  K D P F G F A V F N Y D D V M K K Y E E F V C K W K Q V G Q P K L  597

Sp_Tip1p  585  Y F V R I D I K S C Y D R I K Q D L M F R I V K K K L K D P E - F  616
Sc_Est2p  525  Y F M K F D V K S C Y D S I P R M E C M R I L K D A L K N E N G F  557
Ea_p123   598  F F A T M D I E K C Y D S V N R E K L S T F L K T T K L L S S D F  630

Sp_Tip1p  617  V I R K Y A T I H A T S D R A T K N - - - - - - - - - - - - - - -  634
Sc_Est2p  558  F V R S Q Y F F N T N T G - - - - - - - - - - - - - - - - - - - -  570
Ea_p123   631  W I M T A Q I L K R K N N I V I D S K N F R K K E M K D Y F R Q K  663
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p  635  FVSEAFSYFDMVPFEKVVQLLS--MKTSDTLFV  665
Sc_Est2p  571  -----------VLKLFNVVNASR--VPKPYELYI  591
Ea_p123   664  FQKIALEGGQYPTLFSVLENEQNDLNAKKTLIV  696

Sp_Tip1p  666  DFVDYWTKSSSEIFKMLKEHLSGHIVKIGNSQY  698
Sc_Est2p  592  DNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  624
Ea_p123   697  EAKQRNYFKKDNLLQPVINICQYNYINFNGKFY  729

Sp_Tip1p  699  LQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTK  731
Sc_Est2p  625  IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKA  657
Ea_p123   730  KQTKGIPQGLCVSSILSSFYYATLEESSLGFLR  762

Sp_Tip1p  732  KKG---------SVLLRVVDDFLFITVNKKDAKK  756
Sc_Est2p  658  SPSQD-------TLILKLADDFLIISTDQQQVIN  684
Ea_p123   763  DESMNPENPNVNLLMRLTDDYLLITTQENNAVL  795

Sp_Tip1p  757  FLNLSLRGFEKHNFSTSLEKTVINFENSNG---  786
Sc_Est2p  685  IKKLAMGGFQKYNAKANRDKILAVSSQSD----  713
Ea_p123   796  FIEKLINVSRENGFKFNMKKLQTSFPLSPSKFA  828

Sp_Tip1p  787  ---IINNTFFNESKKRMPFFGFSVNMRSLDTLL  816
Sc_Est2p  714  ----DDTVIQFCA---MHIFVKELEVWKHSSTM  739
Ea_p123   829  KYGMDSVEEQNIVQDYCDWIGISIDMKTLALMP  861

Sp_Tip1p  817  ACPKIDEALFNSTSVELTKHMGKSFFYKILRSS  849
Sc_Est2p  740  NNFHIRSKSSKGIFRSLIALFNTRISYKTIDTN  772
Ea_p123   862  NINLRIEGILCTLNLNMQTKKASMWLKKKLKSF  894
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p   850   LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR   882
Sc_Est2p   773   LNSTNTVLMQIDHVVKNISEC------------   793
Ea_p123    895   LMNNITHYFRKTITTEDFANKTLNKLFISGGYK   927

Sp_Tip1p   883   AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK   915
Sc_Est2p   794   ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM   821
Ea_p123    928   YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV   960

Sp_Tip1p   916   LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS   948
Sc_Est2p   822   TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN   854
Ea_p123    961   TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF   993

Sp_Tip1p   949   FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF   981
Sc_Est2p   855   TS----------KFKDNIILLRKEIQHLQAYIY   877
Ea_p123    994   IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC  1023

Sp_Tip1p   982   LHRRIAD-                            988
Sc_Est2p   878   IYIHIVN-                            884
Ea_p123   1024   QSLIQYDA                           1031
```

FIG. 42
(CONTINUED)

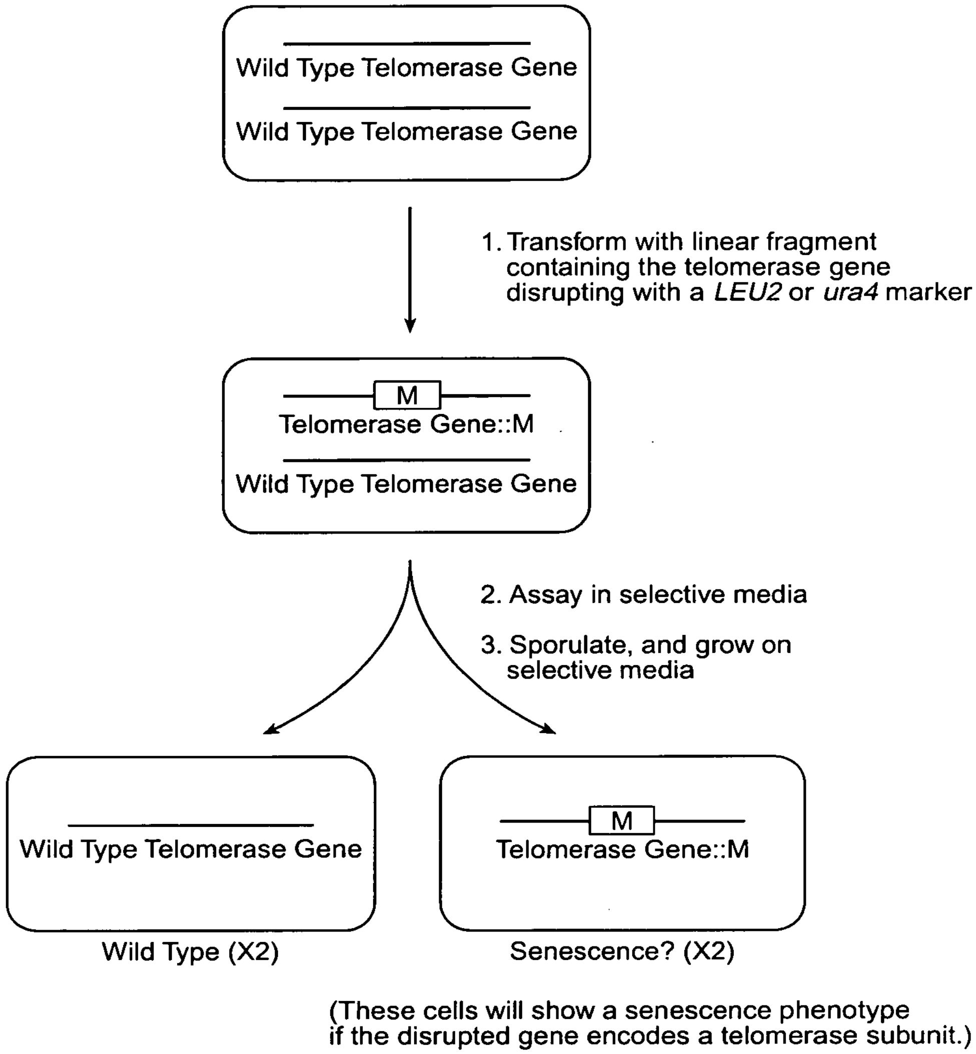

Wild Type Telomerase Gene
Wild Type Telomerase Gene
1. Transform with linear fragment containing the telomerase gene disrupting with a *LEU2* or *ura4* marker
M
Telomerase Gene::M
Wild Type Telomerase Gene
2. Assay in selective media
3. Sporulate, and grow on selective media
Wild Type Telomerase Gene
M
Telomerase Gene::M
Wild Type (X2)
Senescence? (X2)
(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 43

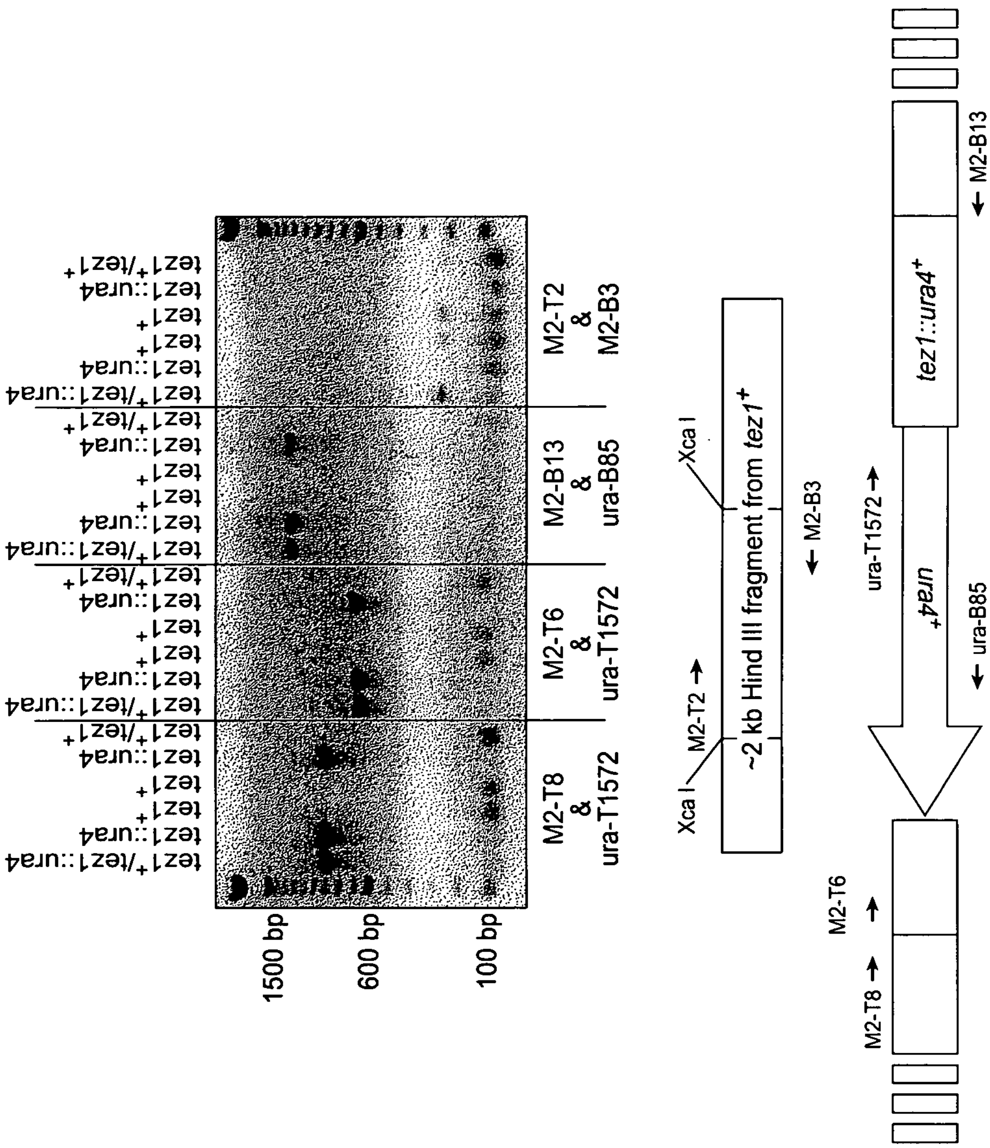

1500 bp
600 bp
100 bp
tez1+/tez1::ura4
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
M2-T8 & ura-T1572
M2-T6 & ura-T1572
M2-B13 & ura-B85
M2-T2 & M2-B3
Xca I
M2-T2
~2 kb Hind III fragment from tez1+
M2-B3
Xca I
M2-T8
M2-T6
ura-T1572
ura4+
ura-B85
tez1::ura4+
M2-B13

FIG. 44

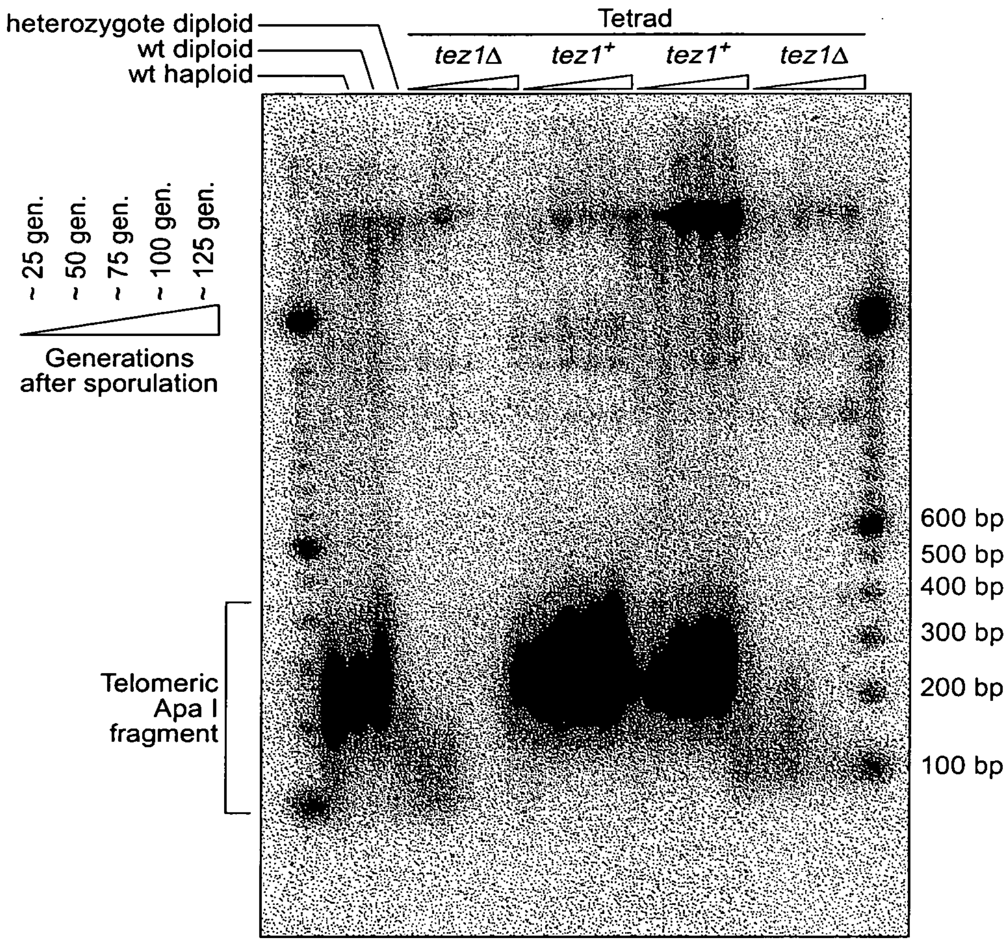

heterozygote diploid
wt diploid
wt haploid
Tetrad
tez1Δ
tez1+
tez1+
tez1Δ
~ 25 gen.
~ 50 gen.
~ 75 gen.
~ 100 gen.
~ 125 gen.
Generations after sporulation
Telomeric Apa I fragment
600 bp
500 bp
400 bp
300 bp
200 bp
100 bp

FIG. 45

20110495001 (stamped, garbled)


```
   1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
  81 actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160
 161 ccaagtataaggacaaaaagaacaacttccttcccccctaaagactttttactttattaatttacttttcaaatatatttcg 240
 241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat 320
 321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc 400
 401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
 481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttttgatgcttgcacacgtctagcatg 560
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctattttctattctcatgttgtt 640
 641 ccaaatatgtatcatctcgtattaggctttttttccgttttactcctggaatcgtaccttttttcactattccccctaatga 720
 721 ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa 800
 801 gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
 881 actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc   958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA  1018
   1 M   T   E   H   H   T   P   K   S   R   I   L   R   F   L   E   N   Q   Y   V    20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG  1078
  21 Y   L   C   T   L   N   D   Y   V   Q   L   V   L   R   G   S   P   A   S   S    40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT  1138
  41 Y   S   N   I   C   E   R   L   R   S   D   V   Q   T   S   F   S   I   F   L    60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA  1198
  61 H   S   T   V   V   G   F   D   S   K   P   D   E   G   V   Q   F   S   S   P    80

1199 AAA TGC TCA CAG TCA GAG gtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcag 1272
  81 K   C   S   Q   S   E                                                            86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA  1332
  87 L   I   A   N   V   V   K   Q   M   F   D   E   S   F   E   R   R   R   N   L    106

1333 CTG ATG AAA GGG TTT TCC ATG gtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405
 107 L   M   K   G   F   S   M                                                        113

1406 ttgtatttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT  1469
 114                     N   H   E   D   F   R   A   M   H   V   N   G   V   Q   N    128
```

FIG. 46

```
1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA  1529
 129 D   L   V   S   T   F   P   N   Y   L   I   S   I   L   E   S   K   N   W   Q    148

1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L   L   L   E   I                                                       I   G    155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC  1661
 156 S   D   A   M   H   Y   L   L   S   K   G   S   I   F   E   A   L   P   N   D    175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG  1721
 176 N   Y   L   Q   I   S   G   I   P   L   F   K   N   N   V   F   E   E   T   V    195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA  1781
 196 S   K   K   R   K   R   T   I   E   T   S   I   T   Q   N   K   S   A   R   K    215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT  1841
 216 E   V   S   W   N   S   I   S   I   S   R   F   S   I   F   Y   R   S   S   Y    235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaattttag AT CTA TAT TTT AAC    1907
 236 K   K   F   K   Q   D                                          L   Y   F   N      245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG  1967
 246 L   H   S   I   C   D   R   N   T   V   H   M   W   L   Q   W   I   F   P   R    265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA  2027
 266 Q   F   G   L   I   N   A   F   Q   V   K   Q   L   H   K   V   I   P   L   V    285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA  2087
 286 S   Q   S   T   V   V   P   K   R   L   L   K   V   Y   P   L   I   E   Q   T    305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT  2147
 306 A   K   R   L   H   R   I   S   L   S   K   V   Y   N   H   Y   C   P   Y   I    325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG  2207
 326 D   T   H   D   D   E   K   I   L   S   Y   S   L   K   P   N   Q   V   F   A    345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA  2267
 346 F   L   R   S   I   L   V   R   V   F   P   K   L   I   W   G   N   Q   R   I    365
```

FIG. 46

(CONTINUED)

```
2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F   E   I   I   L   K   D                                               L   E   T   375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG  2396
 376 F   L   K   L   S   R   Y   E   S   F   S   L   H   Y   L   M   S   N   I   K    395

2397 gtaatatgccaaatttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA  2465
 396                                         I   S   E   I   E   W   L   V   L   G    405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG  2525
 406 K   R   S   N   A   K   M   C   L   S   D   F   E   K   R   K   Q   I   F   A    425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT  2585
 426 E   F   I   Y   W   L   Y   N   S   F   I   I   P   I   L   Q   S   F   F   Y    445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA  2645
 446 I   T   E   S   S   D   L   R   N   R   T   V   Y   F   R   K   D   I   W   K    465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG  2705
 466 L   L   C   R   P   F   I   T   S   M   K   M   E   A   F   E   K   I   N   E    485

2706 gtattttaaagtatttttttgcaaaaagctaatattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486                                            N   N   V   R   M   D   T   Q   K   T   495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG  2835
 496 T   L   P   P   A   V   I   R   L   L   P   K   K   N   T   F   R   L   I   T    515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggtcatcaatgtactttacttctaatctatta 2906
 516 N   L   R   K   R   F   L   I   K                                                524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG  2967
 525        M   G   S   N   K   K   M   L   V   S   T   N   Q   T   L   R   P   V    542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG  3027
 543 A   S   I   L   K   H   L   I   N   E   E   S   S   G   I   P   F   N   L   E    562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V   Y   M   K   L   L   T   F   K   K   D   L   L   K   H   R   M   F   G        581
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FIG. 46
(CONTINUED)

```
3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA   3155
 582                                        R   K   K   Y   F   V   R   I   D   I    591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC  3215
 592 K   S   C   Y   D   R   I   K   Q   D   L   M   F   R   I   V   K   K   K   L    611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT  3275
 612 K   D   P   E   F   V   I   R   K   Y   A   T   I   H   A   T   S   D   R   A    631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttcattggaatttttaacaa 3343
 632 T   K   N   F   V   S   E   A   F   S   Y   F                                    643

3344 attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA  3405
 644                D   M   V   P   F   E   K   V   V   Q   L   L   S   M   K   T    659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT  3465
 660 S   D   T   L   F   V   D   F   V   D   Y   W   T   K   S   S   S   E   I   F    679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532
 680 K   M   L   K   E   H   L   S   G   H   I   V   K                                692

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA     3593
 693               I   G   N   S   Q   Y   L   Q   K   V   G   I   P   Q   G   S      708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG  3653
 709 I   L   S   S   F   L   C   H   F   Y   M   E   D   L   I   D   E   Y   L   S    728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA  3713
 729 F   T   K   K   K   G   S   V   L   L   R   V   V   D   D   F   L   F   I   T    748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
 749 V   N   K   K   D   A   K   K   F   L   N   L   S   L   R   G                    764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA    3840
 765                       F   E   K   H   N   F   S   T   S   L   E   K   T   V     778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA  3900
 779 I   N   F   E   N   S   N   G   I   I   N   N   T   F   F   N   E   S   K   K    798
```

FIG. 46
(CONTINUED)

```
3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT  3960
 799 R   M   P   F   F   G   F   S   V   N   M   R   S   L   D   T   L   L   A   C    818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG  4020
 819 P   K   I   D   E   A   L   F   N   S   T   S   V   E   L   T   K   H   M   G    838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
 839 K   S   F   F   Y   K   I   L   R                                              S    848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT  4149
 849 S   L   A   S   F   A   Q   V   F   I   D   I   T   H   N   S   K   F   N   S    868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA  4209
 869 C   C   N   I   Y   R   L   G   Y   S   M   C   M   R   A   Q   A   Y   L   K    888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
 889 R   M   K   D   I   F   I   P   Q   R   M   F   I   T   D                        903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
 904                         L   L   N   V   I   G   R   K   I   W   K   K   L   A    917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
 918 E   I   L   G   Y   T   S   R   R   F   L   S   S   A   E   V   K   W            935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA  4468
 936                                     L   F   C   L   G   M   R   D   G   L   K    946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT  4528
 947 P   S   F   K   Y   H   P   C   F   E   Q   L   I   Y   Q   F   Q   S   L   T    966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA  4588
 967 D   L   I   K   P   L   R   P   V   L   R   Q   V   L   F   L   H   R   R   I    986

4589 GCT GAT TAA tgtcattttcaatttattatatacatcctttattactggtgtcttaaacaatattattactaagtata 4665
 987 A   D   *                                                                        989
```

FIG. 46
(CONTINUED)

```
4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta 5145
5146 atgtcttatataaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc  5544
```

FIG. 46
(CONTINUED)

```
                         1
                        met ser val tyr val val glu leu leu
GCCAAGTTCCTGCACTGGCTG   ATG AGT GTG TAC GTC GTC GAG CTG CTC

 10                                         20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

                     30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

 40                                         50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

                     60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

 70                                         80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

                     90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100                                         110
glu lys     ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

                    120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130                                         140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

                    150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160                                         170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

                    180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190                                         200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG
```

FIG. 47

```
                    210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220                                     230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

                    240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250                                     260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

                    270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280                                     290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

                    300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310                                     320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

                    330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340                                     350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

                    360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370                                     380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

                    390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400                                     410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG
```

FIG. 47
(CONTINUED)

420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT

CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCTTCGCCCTGCCTTCC

TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG

AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG

GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT

TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 47
(CONTINUED)

```
Motif -1
Ep p123        ...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1        ...FIIPILQSFFYITESSDLRNRT...
Sc Est2        ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1        ...YVVELLRSFFYVTETTFQKNRL...
consensus                 FFY TE

                                                 K
Motif 0                  p hhh  K     hR h       R
Ep p123        ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1        ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
Sc Est2        ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1        ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus                    R  PK      R I

                              AF
Motif A               h  hDh  GY  h
Ep p123        ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1        ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2        ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1        ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus             F   D    YD

Motif B                     hPQG  pS  hh
Ep p123        ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1        ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2        ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1        ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus                  G  QG   S

                          Y
Motif C                h  F DD hhh
Ep p123        ...PNVNLLMRLTDDYLLITTQENN...
Sp Tez1        ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2        ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1        ...RRDGLLLRLVDDFLLVTPHLTH...
consensus                   DD L

Motif D                 Gh h  cK
Ep p123        ...NVSRENGFKFNMKKL...
Sp Tez1        ...LNLSLRGFEKHNFST...
Sc Est2        ...KKLAMGGFQKYNAKA...
Hs TCP1        ...LRTLVRGVPEYGCVV...
consensus               G
```

FIG. 48

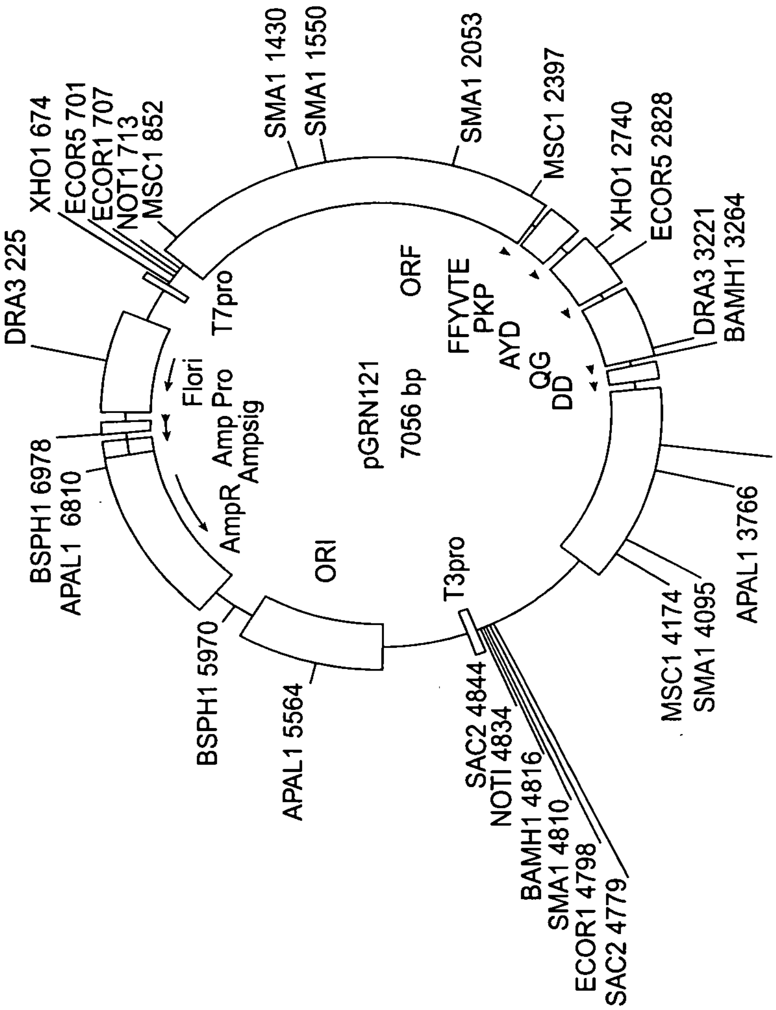

pGRN121
7056 bp
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
SMA1 1430
SMA1 1550
SMA1 2053
MSC1 2397
XHO1 2740
ECOR5 2828
DRA3 3221
BAMH1 3264
SAC2 3658
APAL1 3766
SMA1 4095
MSC1 4174
SAC2 4844
NOTI 4834
BAMH1 4816
SMA1 4810
ECOR1 4798
SAC2 4779
APAL1 5564
BSPH1 5970
APAL1 6810
BSPH1 6978
DRA3 225
T7pro
T3pro
ORF
FFYVTE
PKP
AYD
QG
DD
Flori
Amp Pro
Ampsig
AmpR
ORI

FIG. 49

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC
401 ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
501 TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC
551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
801 CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT
851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG
1101 AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG
1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA
2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
2251 AACCCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC
2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC

FIG. 50

2501	CGTGCGCATC	AGGGGCAAGT	CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG
2551	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	TGTGCTACGG	CGACATGGAG
2601	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	TGCGTTTGGT
2651	GGATGATTTC	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC
2701	TCAGGACCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACTTG
2751	CGGAAGACAG	TGGTGAACTT	CCCTGTAGAA	GACGAGGCCC	TGGGTGGCAC
2801	GGCTTTTGTT	CAGATGCCGG	CCCACGGCCT	ATTCCCCTGG	TGCGGCCTGC
2851	TGCTGGATAC	CCGGACCCTG	GAGGTGCAGA	GCGACTACTC	CAGCTATGCC
2901	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	TCAAGGCTGG
2951	GAGGAACATG	CGTCGCAAAC	TCTTTGGGGT	CTTGCGGCTG	AAGTGTCACA
3001	GCCTGTTTCT	GGATTTGCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC
3051	ATCTACAAGA	TCCTCCTGCT	GCAGGCGTAC	AGGTTTCACG	CATGTGTGCT
3101	GCAGCTCCCA	TTTCATCAGC	AAGTTTGGAA	GAACCCCACA	TTTTTCCTGC
3151	GCGTCATCTC	TGACACGGCC	TCCCTCTGCT	ACTCCATCCT	GAAAGCCAAG
3201	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	CTCTGCCCTC
3251	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATTCCTGCTC	AAGCTGACTC
3301	GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCCAG
3351	ACGCAGCTGA	GTCGGAAGCT	CCCGGGGACG	ACGCTGACTG	CCCTGGAGGC
3401	CGCAGCCAAC	CCGGCACTGC	CCTCAGACTT	CAAGACCATC	CTGGACTGAT
3451	GGCCACCCGC	CCACAGCCAG	GCCGAGAGCA	GACACCAGCA	GCCCTGTCAC
3501	GCCGGGCTCT	ACGTCCCAGG	GAGGGAGGGG	CGGCCCACAC	CCAGGCCCGC
3551	ACCGCTGGGA	GTCTGAGGCC	TGAGTGAGTG	TTTGGCCGAG	GCCTGCATGT
3601	CCGGCTGAAG	GCTGAGTGTC	CGGCTGAGGC	CTGAGCGAGT	GTCCAGCCAA
3651	GGGCTGAGTG	TCCAGCACAC	CTGCCGTCTT	CACTTCCCCA	CAGGCTGGCG
3701	CTCGGCTCCA	CCCCAGGGCC	AGCTTTTCCT	CACCAGGAGC	CCGGCTTCCA
3751	CTCCCCACAT	AGGAATAGTC	CATCCCCAGA	TTCGCCATTG	TTCACCCCTC
3801	GCCCTGCCCT	CCTTTGCCTT	CCACCCCCAC	CATCCAGGTG	GAGACCCTGA
3851	GAAGGACCCT	GGGAGCTCTG	GGAATTTGGA	GTGACCAAAG	GTGTGCCCTG
3901	TACACAGGCG	AGGACCCTGC	ACCTGGATGG	GGGTCCCTGT	GGGTCAAATT
3951	GGGGGGAGGT	GCTGTGGGAG	TAAAATACTG	AATATATGAG	TTTTTCAGTT
4001	TTGAAAAAAA	AAAAAAAAAA	AAAAAAAAA		

FIG. 50
(CONTINUED)

```
      GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC
    1 ---------+---------+---------+---------+---------+---------+ 60
      CGTCGCGACGCAGGACGACGCGTGCACCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGG

a      A  A  L  R  P  A  A  H  V  G  S  P  G  P  G  H  P  R  D  A   -
b       Q  R  C  V  L  L  R  T  W  E  A  L  A  P  A  T  P  A  M  P  -
c        S  A  A  S  C  C  A  R  G  K  P  W  P  R  P  P  P  R  C  R -

      GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
   61 ---------+---------+---------+---------+---------+---------+ 120
      CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGA

a      A  R  S  P  L  P  S  R  A  L  P  A  A  Q  P  L  P  R  G  A   -
b       R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  -
c        A  L  P  A  A  E  P  C  A  P  C  C  A  A  T  T  A  R  C  C -

      GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
  121 ---------+---------+---------+---------+---------+---------+ 180
      CGGCGACCGGTGCAAGCACGCCGCGGACCCCGGGGTCCCGACCGCCGACCACGTCGCGCC

a      A  A  G  H  V  R  A  A  P  G  A  P  G  L  A  A  G  A  A  R   -
b       P  L  A  T  F  V  R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  -
c        R  W  P  R  S  C  G  A  W  G  P  R  A  G  G  W  C  S  A  G -

      GGACCCGGCGGCTTTCCGCGCGNTGGTGGCCCANTGCNTGGTGTGCGTGCCCTGGGANGN
  181 ---------+---------+---------+---------+---------+---------+ 240
      CCTGGGCCGCCGAAAGGCGCGCNACCACCGGGTNACGNACCACACGCACGGGACCCTNCN

a      G  P  G  G  F  P  R  ?  G  G  P  ?  ?  G  V  R  A  L  G  ?   -
b       D  P  A  A  F  R  A  ?  V  A  ?  C  ?  V  C  V  P  W  ?  ?  -
c        T  R  R  L  S  A  R  W  W  P  ?  A  W  C  A  C  P  G  ?  ? -

      ANGGCNGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAANGANCTGGTGGC
  241 ---------+---------+---------+---------+---------+---------+ 300
      TNCCGNCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACAGGACGGACTTNCTNGACCACCG

a      ?  A  A  P  R  R  P  L  L  P  P  G  V  L  P  E  ?  ?  G  G   -
b       ?  ?  P  P  A  A  P  S  F  R  Q  V  S  C  L  ?  ?  L  V  A  -
c        G  ?  P  P  P  P  P  P  S  A  R  C  P  A  *  ?  ?  W  W  P -

      CCGAGTGCTGCANANGCTGTGCGANCGCGGCGCGAANAACGTGCTGGCCTTCGGCTTCGC
  301 ---------+---------+---------+---------+---------+---------+ 360
      GGCTCACGACGTNTNCGACACGCTNGCGCCGCGCTTNTTGCACGACCGGAAGCCGAAGCG

a      P  S  A  A  ?  A  V  R  ?  R  R  E  ?  R  A  G  L  R  L  R   -
b       R  V  L  ?  ?  L  C  ?  R  G  A  ?  N  V  L  A  F  G  F  A  -
c        E  C  C  ?  ?  C  A  ?  A  A  R  ?  T  C  W  P  S  A  S  R -

      GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA
  361 ---------+---------+---------+---------+---------+---------+ 420
      CGACGACCTGCCCCGGGCGCCCCCGGGGGGGCTCCGGAAGTGGTGGTCGCACGCGTCGAT

a      A  A  G  R  G  P  R  G  P  P  R  G  L  H  H  Q  R  A  Q  L   -
b       L  L  D  G  A  R  G  G  P  P  E  A  F  T  T  S  V  R  S  Y  -
c        C  W  T  G  P  A  G  A  P  P  R  P  S  P  P  A  C  A  A  T -

      CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG
  421 ---------+---------+---------+---------+---------+---------+ 480
      GGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTCGCCCCGCACCCCCGACGACGACGC

a      P  A  Q  H  G  D  R  R  T  A  G  E  R  G  V  G  A  A  A  A   -
b       L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  R  -
c        C  P  T  R  *  P  T  H  C  G  G  A  G  R  G  G  C  C  C  A -
```

FIG. 51

```
a        P  R  G  R  R  R  A  G  S  P  A  G  T  L  R  ?  ?  C  A  G  -
b         R  V  G  D  D  V  L  V  H  L  L  A  R  C  A  ?  F  V  L  V  -
c          A  W  A  T  T  C  W  F  T  C  W  H  A  A  R  ?  L  C  W  W -

         GGNTCCCAGCTGCGCCTACCANGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCNAC
     541 ---------+---------+---------+---------+---------+---------+ 600
         CCNAGGGTCGACGCGGATGGTNCACACGCCCGGCGGCGACATGGTCGAGCCGCGACGNTG

a        G  S  Q  L  R  L  P  ?  V  R  A  A  A  V  P  A  R  R  C  ?  -
b         ?  P  S  C  A  Y  ?  V  C  G  P  P  L  Y  Q  L  G  A  A  T  -
c          ?  P  A  A  P  T  ?  C  A  G  R  R  C  T  S  S  A  L  ?  L -

         TCAGGCCCGGCCCCCGCCACACGCTANTGGACCCGAANGCGTCTGGGATCCAACGGGCCT
     601 ---------+---------+---------+---------+---------+---------+ 660
         AGTCCGGGCCGGGGGCGGTGTGCGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCGGA

a        S  G  P  A  P  A  T  R  ?  W  T  R  ?  R  L  G  S  N  G  P  -
b         Q  A  R  P  P  P  H  A  ?  G  P  E  ?  V  W  D  P  T  G  L  -
c          R  P  G  P  R  H  T  L  ?  D  P  ?  A  S  G  I  Q  R  A  W -

         GGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAG
     661 ---------+---------+---------+---------+---------+---------+ 720
         CCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCCGACGGTCGGGGCCCACGCTCCTC

a        G  T  I  A  S  G  R  P  G  S  P  W  A  A  S  P  G  C  E  E  -
b         E  P  *  R  Q  G  G  R  G  P  P  G  L  P  A  P  G  A  R  R  -
c          N  H  S  V  R  E  A  G  V  P  L  G  C  Q  P  R  V  R  G  G -

         GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGC
     721 ---------+---------+---------+---------+---------+---------+ 780
         CGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGGGTTCTCCGGGTCCGCACCGCGACG

a        A  R  G  Q  C  Q  P  K  S  A  V  A  Q  E  A  Q  A  W  R  C  -
b         R  G  G  S  A  S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  -
c          A  G  A  V  P  A  E  V  C  R  C  P  R  G  P  G  V  A  L  P -

         CCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGCCCACCCGGGCAGGACGCC
     781 ---------+---------+---------+---------+---------+---------+ 840
         GGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCGTCCTGCGG

a        P  *  A  G  A  D  A  R  W  A  G  V  L  G  P  P  G  Q  D  A  -
b         P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  P  -
c          L  S  R  S  G  R  P  L  G  R  G  P  G  P  T  R  A  G  R  L -

         TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGCCAC
     841 ---------+---------+---------+---------+---------+---------+ 900
         ACCTGGCTCACTGGCACCAAAGACACACCACAGTGGACGGTCTGGGCGGCTTCTTCGGTG

a        W  T  E  *  P  W  F  L  C  G  V  T  C  Q  T  R  R  R  S  H  -
b         G  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E  A  T  -
c          D  R  V  T  V  V  S  V  W  C  H  L  P  D  P  P  K  K  P  P -

         CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCA
     901 ---------+---------+---------+---------+---------+---------+ 960
         GAGAAACCTCCCACGCGAGAGACCGTGCGCGGTGAGGGTGGGTAGGCACCCGGCGGTCGT

a        L  F  G  G  C  A  L  W  H  A  P  L  P  P  I  R  G  P  P  A  -
b         S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  -
c          L  W  R  V  R  S  L  A  R  A  T  P  T  H  P  W  A  A  S  T -

         CCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCCTTGTCCCCCG
     961 ---------+---------+---------+---------+---------+---------+ 1020
         GGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC
```

FIG. 51
(CONTINUED)

```
a        P  R  G  P  P  I  H  I  A  A  T  T  S  W  D  T  P  C  P  P  -
b         H  A  G  P  P  S  T  S  R  P  P  R  P  G  T  R  L  V  P  R -
c          T  R  A  P  H  P  H  R  G  H  H  V  L  G  H  A  L  S  P  G-

         GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
    1021 ---------+---------+---------+---------+---------+---------+ 1080
         CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCNTGTGACGCNGGGAG

a        V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  ?  T  A  ?  L  -
b         C  T  P  R  P  S  T  S  S  T  P  Q  A  T  ?  T  L  R  P  S -
c          V  R  R  D  Q  A  L  P  L  L  L  R  R  Q  ?  H  C  ?  P  P-

         CTTCCTACTCAATATATCTGAGGCCCAGCCTGACTGGCGTTCGGGAGGTTCGTGGAGACA
    1081 ---------+---------+---------+---------+---------+---------+ 1140
         GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a        L  P  T  Q  Y  I  *  G  P  A  *  L  A  F  G  R  F  V  E  T  -
b         F  L  L  N  I  S  E  A  Q  P  D  W  R  S  G  G  S  W  R  ? -
c          S  Y  S  I  Y  L  R  P  S  L  T  G  V  R  E  V  R  G  D  ?-

         NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCCCGCAGGTTGCCCCGCCTGCCCCA
    1141 ---------+---------+---------+---------+---------+---------+ 1200
         NAGAAAGACCAAGGTCCGGAACCTACGGTCCTAAGGGGCGTCCAACGGGGCGGACGGGGT

a        ?  F  L  V  P  G  L  G  C  Q  D  S  P  Q  V  A  P  P  A  P  -
b         S  F  W  F  Q  A  L  D  A  R  I  P  R  R  L  P  R  L  P  Q -
c          L  S  G  S  R  P  W  M  P  G  F  P  A  G  C  P  A  C  P  S-

         GCGNTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCC
    1201 ---------+---------+---------+---------+---------+---------+ 1260
         CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCTTGGTGCGCGTCACGGG

a        A  ?  L  A  N  A  A  P  V  S  G  A  A  W  E  P  R  A  V  P  -
b         R  Y  W  Q  M  R  P  L  F  L  E  L  L  G  N  H  A  Q  C  P -
c          ?  T  G  K  C  G  P  C  F  W  S  C  L  G  T  T  R  S  A  P-

         CTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGG
    1261 ---------+---------+---------+---------+---------+---------+ 1320
         GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTCGGCC

a        L  R  G  V  P  Q  D  A  L  P  A  A  S  C  G  H  P  S  S  R  -
b         Y  G  V  F  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G -
c          T  G  C  S  S  R  R  T  A  R  C  E  L  R  S  P  Q  Q  P  V-

         TGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGAACACAG
    1321 ---------+---------+---------+---------+---------+---------+ 1380
         ACAGACACGGGCCCTCTTCGGGGTCCCGAGACACCGCCGGGGGCTCCTCCTCCTTGTGTC

a        C  L  C  P  G  E  A  P  G  L  C  G  G  P  R  G  G  G  T  Q  -
b         V  C  A  R  E  K  P  Q  G  S  V  A  A  P  E  E  E  E  H  R -
c          S  V  P  G  R  S  P  R  A  L  W  R  P  P  R  R  R  N  T  D-

         ACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
    1381 ---------+---------+---------+---------+---------+---------+ 1440
         TGGGGGCAGCGGACCACGTCGACGAGGCGGTCGTGTCGTCGGGGACCGTCCACATGCCGA

a        T  P  V  A  W  C  S  C  S  A  S  T  A  A  P  G  R  C  T  A  -
b         P  P  S  P  G  A  A  A  P  P  A  Q  Q  P  L  A  G  V  R  L -
c          P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F-

         TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACG
    1441 ---------+---------+---------+---------+---------+---------+ 1500
         AGCACGCCCGGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCCGAGGTCCGTGTTGC
```

FIG. 51
(CONTINUED)

```
a        S  C  G  P  A  C  A  G  W  C  P  Q  A  S  G  A  P  G  T  T  -
b         R  A  G  L  P  A  P  A  G  A  P  R  P  L  G  L  Q  A  Q  R  -
c          V  R  A  C  L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E -

         AACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT
    1501 ---------+---------+---------+---------+---------+---------+ 1560
         TTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA

a        N  A  A  S  S  G  T  P  R  S  S  S  P  W  G  S  M  P  S  S  -
b         T  P  L  P  Q  E  H  Q  E  V  H  L  P  G  E  A  C  Q  A  L  -
c          R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  K  L  S -

         CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCC
    1561 ---------+---------+---------+---------+---------+---------+ 1620
         GCGACGTCCTCGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGCGTCCTCGG

a        R  C  R  S  *  R  G  R  *  A  C  G  T  A  L  G  C  A  G  A  -
b         A  A  G  A  D  V  E  D  E  R  A  G  L  R  L  A  A  Q  E  P  -
c          L  Q  E  L  T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P -

         CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
    1621 ---------+---------+---------+---------+---------+---------+ 1680
         GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGGTTCA

a        Q  G  L  A  V  F  R  P  Q  S  T  V  C  V  R  R  S  W  P  S  -
b         R  G  W  L  C  S  G  R  R  A  P  S  A  *  G  D  P  G  Q  V  -
c          G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F -

         TCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCA
    1681 ---------+---------+---------+---------+---------+---------+ 1740
         AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAAGAAAATACAGT

a        S  C  T  G  *  *  V  C  T  S  S  S  C  S  G  L  S  F  M  S  -
b         P  A  L  A  D  E  C  V  R  R  R  A  A  Q  V  F  L  L  C  H  -
c          L  H  W  L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T -

         CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
    1741 ---------+---------+---------+---------+---------+---------+ 1800
         GCCTCTGGTGCAAAGTTTTCTTGTCCGAGAAAAAGATGGCCTTCTCACAGACCTCGTTCA

a        R  R  P  R  F  K  R  T  G  S  F  S  T  G  R  V  S  G  A  S  -
b         G  D  H  V  S  K  E  Q  A  L  F  L  P  E  E  C  L  E  Q  V  -
c          E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L -

         TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG
    1801 ---------+---------+---------+---------+---------+---------+ 1860
         ACGTTTCGTAACCTTAGTCTGTCGTGAACTTCTCCCACGTCGACGCCCTCGACAGCCTTC

a        C  K  A  L  E  S  D  S  T  *  R  G  C  S  C  G  S  C  R  K  -
b         A  K  H  W  N  Q  T  A  L  E  E  G  A  A  A  G  A  V  G  S  -
c          Q  S  I  G  I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A -

         CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA
    1861 ---------+---------+---------+---------+---------+---------+ 1920
         GTCTCCAGTCCGTCGTAGCCCTTCGGTCCGGGCGGGACGACTGCAGGTCTGAGGCGAAGT

a        Q  R  S  G  S  I  G  K  P  G  P  P  C  *  R  P  D  S  A  S  -
b         R  G  Q  A  A  S  G  S  Q  A  R  P  A  D  V  Q  T  P  L  H  -
c          E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I -

         TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA
    1921 ---------+---------+---------+---------+---------+---------+ 1980
         AGGGGTTCGGACTGCCCGACGCCGGCTAACACTTGTACCTGATGCAGCACCCTCGGTCTT
```

FIG. 51
(CONTINUED)

```
a        S  P  S  L  T  G  C  G  R  L  *  T  W  T  T  S  W  E  P  E   -
b         P  Q  A  *  R  A  A  A  D  C  E  H  G  L  R  R  G  S  Q  N  -
c          P  K  P  D  G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T -

         CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCG
   1981  ---------+---------+---------+---------+---------+---------+ 2040
         GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC

a        R  S  A  E  K  R  G  P  S  V  S  P  R  G  *  R  H  C  S  A   -
b         V  P  Q  R  K  E  G  R  A  S  H  L  E  G  E  G  T  V  Q  R  -
c          F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V -

         TGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGG
   2041  ---------+---------+---------+---------+---------+---------+ 2100
         ACGAGTTGATGCTCGCCCGCGCCGCGGGGCCGGAGGACCCGCGGAGACACGACCCGGACC

a        C  S  T  T  S  G  R  G  A  P  A  S  W  A  P  L  C  W  A  W   -
b         A  Q  L  R  A  G  A  A  P  R  P  P  G  R  L  C  A  G  P  G  -
c          L  N  Y  E  R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D -

         ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGC
   2101  ---------+---------+---------+---------+---------+---------+ 2160
         TGCTATAGGTGTCCCGGACCGCGTGGAAGCACGACGCACACGCCCGGGTCCTGGGCGGCG

a        T  I  S  T  G  P  G  A  P  S  C  C  V  C  G  P  R  T  R  R   -
b         R  Y  P  Q  G  L  A  H  L  R  A  A  C  A  G  P  G  P  A  A  -
c          D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P -

         CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACA
   2161  ---------+---------+---------+---------+---------+---------+ 2220
         GACTCGACATGAAACAGTTCCACCTACACTGCCCGCGCATGCTGTGGTAGGGGGTCCTGT

a        L  S  C  T  L  S  R  W  M  *  R  A  R  T  T  P  S  P  R  T   -
b         *  A  V  L  C  Q  G  G  C  D  G  R  V  R  H  H  P  P  G  Q  -
c          E  L  Y  F  V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R -

         GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT
   2221  ---------+---------+---------+---------+---------+---------+ 2280
         CCGAGTGCCTCCAGTAGCGGTCGTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA

a        G  S  R  R  S  S  P  A  S  S  N  P  R  T  R  T  A  C  V  G   -
b         A  H  G  G  H  R  Q  H  H  Q  T  P  E  H  V  L  R  A  S  V  -
c          L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y -

         ATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT
   2281  ---------+---------+---------+---------+---------+---------+ 2340
         TACGGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA

a        M  P  W  S  R  R  P  P  M  G  T  S  A  R  P  S  R  A  T  S   -
b         C  R  G  P  E  G  R  P  W  A  R  P  Q  G  L  Q  E  P  R  L  -
c          A  V  V  Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S -

         CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA
   2341  ---------+---------+---------+---------+---------+---------+ 2400
         GATGGAACTGTCTGGAGGTCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCCTNTTGT

a        L  P  *  Q  T  S  S  R  T  C  D  S  S  W  L  T  C  R  ?  T   -
b         Y  L  D  R  P  P  A  V  H  A  T  V  R  G  S  P  A  G  ?  Q  -
c          T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  ?  N  S -

         GCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
   2401  ---------+---------+---------+---------+---------+---------+ 2460
         CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCGTCAC
```

FIG. 51
(CONTINUED)

```
a        A  R  *  G  M  P  S  S  S  S  R  A  P  P  *  M  R  P  A  V   -
b         P  A  E  G  C  R  R  H  R  A  E  L  L  P  E  *  G  Q  Q  W  -
c          P  L  R  D  A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G -

         GCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGT
    2461 ---------+---------+---------+---------+---------+---------+ 2520
         CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGCGGCACGCGTAGTCCCCGTTCA

a        A  S  S  T  S  S  Y  A  S  C  A  T  T  P  C  A  S  G  A  S   -
b         P  L  R  R  L  P  T  L  H  V  P  P  R  R  A  H  Q  G  Q  V  -
c          L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S -

         CCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
    2521 ---------+---------+---------+---------+---------+---------+ 2580
         GGATGCAGGTCACGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCGG

a        P  T  S  S  A  R  G  S  R  R  A  P  S  S  P  R  C  S  A  A   -
b         L  R  P  V  P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P  -
c          Y  V  Q  C  Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L -

         TGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCC
    2581 ---------+---------+---------+---------+---------+---------+ 2640
         ACACGATGCCGCTGTACCTCTTGTTCGACAAACGCCCCTAAGCCGCCCTGCCCGACGAGG

a        C  A  T  A  T  W  R  T  S  C  L  R  G  F  G  G  T  G  C  S   -
b         V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P  -
c          C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L -

         TGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCC
    2641 ---------+---------+---------+---------+---------+---------+ 2700
         ACGCAAACCACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGGAAGG

a        C  V  W  W  M  I  S  C  W  *  H  L  T  S  P  T  R  K  P  S   -
b         A  F  G  G  *  F  L  V  G  D  T  S  P  H  P  R  E  N  L  P  -
c          R  L  V  D  D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L -

         TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAG
    2701 ---------+---------+---------+---------+---------+---------+ 2760
         AGTCCTGGGACCAGGCTCCACAGGGACTCATACCGACGCACCACTTGAACGCCTTCTGTC

a        S  G  P  W  S  E  V  S  L  S  M  A  A  W  *  T  C  G  R  Q   -
b         Q  D  P  G  P  R  C  P  *  V  W  L  R  G  E  L  A  E  D  S  -
c          R  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V -

         TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
    2761 ---------+---------+---------+---------+---------+---------+ 2820
         ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC

a        W  *  T  S  L  *  K  T  R  P  W  V  A  R  L  L  F  R  C  R   -
b         G  E  L  P  C  R  R  R  G  P  G  W  H  G  F  C  S  D  A  G  -
c          V  N  F  P  V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A -

         CCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGA
    2821 ---------+---------+---------+---------+---------+---------+ 2880
         GGGTGCCGGATAAGGGGACCACGCCGGACGACGACCTATGGGCCTGGGACCTCCACGTCT

a        P  T  A  Y  S  P  G  A  A  C  C  W  I  P  G  P  W  R  C  R   -
b         P  R  P  I  P  L  V  R  P  A  A  G  Y  P  D  P  G  G  A  E  -
c          H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S -

         GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT
    2881 ---------+---------+---------+---------+---------+---------+ 2940
         CGCTGATGAGGTCGATACGGGCCTGGAGGTAGTCTCGGTCAGAGTGGAAGTTGGCGCCGA
```

FIG. 51
(CONTINUED)

```
a        A  T  T  P  A  M  P  G  P  P  S  E  P  V  S  P  S  T  A  A   -
b         R  L  L  Q  L  C  P  D  L  H  Q  S  Q  S  H  L  Q  P  R  L  -
c          D  Y  S  S  Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F -

         TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA
    2941 ---------+---------+---------+---------+---------+---------+ 3000
         AGTTCCGACCCTCCTTGTACGCAGCGTTTGAGAAACCCCAGAACGCCGACTTCACAGTGT

a        S  R  L  G  G  T  C  V  A  N  S  L  G  S  C  G  *  S  V  T   -
b         Q  G  W  E  E  H  A  S  Q  T  L  W  G  L  A  A  E  V  S  Q  -
c          K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S -

         GCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
    3001 ---------+---------+---------+---------+---------+---------+ 3060
         CGGACAAAGACCTAAACGTCCACTTGTCGGAGGTCTGCCACACGTGGTTGTAGATGTTCT

a        A  C  F  W  I  C  R  *  T  A  S  R  R  C  A  P  T  S  T  R   -
b         P  V  S  G  F  A  G  E  Q  P  P  D  G  V  H  Q  H  L  Q  D  -
c          L  F  L  D  L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I -

         TCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
    3061 ---------+---------+---------+---------+---------+---------+ 3120
         AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG

a        S  S  C  C  R  R  T  G  F  T  H  V  C  C  S  S  H  F  I  S   -
b         P  P  A  A  G  V  Q  V  S  R  M  C  A  A  A  P  I  S  S  A  -
c          L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q -

         AAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
    3121 ---------+---------+---------+---------+---------+---------+ 3180
         TTCAAACCTTCTTGGGGTGTAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA

a        K  F  G  R  T  P  H  F  S  C  A  S  S  L  T  R  P  P  S  A   -
b         S  L  E  E  P  H  I  F  P  A  R  H  L  *  H  G  L  P  L  L  -
c          V  W  K  N  P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y -

         ACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCC
    3181 ---------+---------+---------+---------+---------+---------+ 3240
         TGAGGTAGGACTTTCGGTTCTTGCGTCCCTACAGCGACCCCCGGTTCCCGCGGCGGCCGG

a        T  P  S  *  K  P  R  T  Q  G  C  R  W  G  P  R  A  P  P  A   -
b         L  H  P  E  S  Q  E  R  R  D  V  A  G  G  Q  G  R  R  R  P  -
c          S  I  L  K  A  K  N  A  G  M  S  L  G  A  K  G  A  A  G  P -

         CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
    3241 ---------+---------+---------+---------+---------+---------+ 3300
         GAGACGGGAGGCTCCGGCACGTCACCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG

a        L  C  P  P  R  P  C  S  G  C  A  T  K  H  S  C  S  S  *  L   -
b         S  A  L  R  G  R  A  V  A  V  P  P  S  I  P  A  Q  A  D  S  -
c          L  P  S  E  A  V  Q  W  L  C  H  Q  A  F  L  L  K  L  T  R -

         GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGA
    3301 ---------+---------+---------+---------+---------+---------+ 3360
         CTGTGGCACAGTGGATGCACGGTGAGGACCCCAGTGAGTCCTGTCGGGTCTGCGTCGACT

a        D  T  V  S  P  T  C  H  S  W  G  H  S  G  Q  P  R  R  S  *   -
b         T  P  C  H  L  R  A  T  P  G  V  T  Q  D  S  P  D  A  A  E  -
c          H  R  V  T  Y  V  P  L  L  G  S  L  R  T  A  Q  T  Q  L  S -

         GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGC
    3361 ---------+---------+---------+---------+---------+---------+ 3420
         CAGCCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG
```

FIG. 51
(CONTINUED)

```
a        V  G  S  S  R  G  R  R  *  L  P  W  R  P  Q  P  T  R  H  C  -
b         S  E  A  P  G  D  D  A  D  C  P  G  G  R  S  Q  P  G  T  A  -
c          R  K  L  P  G  T  T  L  T  A  L  E  A  A  A  N  P  A  L  P -

         CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCA
    3421 ---------+---------+---------+---------+---------+---------+ 3480
         GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCGGTCCGGCTCTCGT

a        P  Q  T  S  R  P  S  W  T  D  G  H  P  P  T  A  R  P  R  A  -
b         L  R  L  Q  D  H  P  G  L  M  A  T  R  P  Q  P  G  R  E  Q  -
c          S  D  F  K  T  I  L  D  *  W  P  P  A  H  S  Q  A  E  S  R -

         GACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACAC
    3481 ---------+---------+---------+---------+---------+---------+ 3540
         CTGTGGTCGTCGGGACAGTGCGGCCCGAGATGCAGGGTCCCTCCCTCCCCGCCGGGTGTG

a        D  T  S  S  P  V  T  P  G  S  T  S  Q  G  G  R  G  G  P  H  -
b         T  P  A  A  L  S  R  R  A  L  R  P  R  E  G  G  A  A  H  T  -
c          H  Q  Q  P  C  H  A  G  L  Y  V  P  G  R  E  G  R  P  T  P -

         CCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGT
    3541 ---------+---------+---------+---------+---------+---------+ 3600
         GGTCCGGGCGTGGCGACCCTCAGACTCCGGACTCACTCACAAACCGGCTCCGGACGTACA

a        P  G  P  H  R  W  E  S  E  A  *  V  S  V  W  P  R  P  A  C  -
b         Q  A  R  T  A  G  S  L  R  P  E  *  V  F  G  R  G  L  H  V  -
c          R  P  A  P  L  G  V  *  G  L  S  E  C  L  A  E  A  C  M  S -

         CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG
    3601 ---------+---------+---------+---------+---------+---------+ 3660
         GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCGGTTCCCGACTCAC

a        P  A  E  G  *  V  S  G  *  G  L  S  E  C  P  A  K  G  *  V  -
b         R  L  K  A  E  C  P  A  E  A  *  A  S  V  Q  P  R  A  E  C  -
c          G  *  R  L  S  V  R  L  R  P  E  R  V  S  S  Q  G  L  S  V -

         TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCC
    3661 ---------+---------+---------+---------+---------+---------+ 3720
         AGGTCGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG

a        S  S  T  P  A  V  F  T  S  P  Q  A  G  A  R  L  H  P  R  A  -
b         P  A  H  L  P  S  S  L  P  H  R  L  A  L  G  S  T  P  G  P  -
c          Q  H  T  C  R  L  H  F  P  T  G  W  R  S  A  P  P  Q  G  Q -

         AGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
    3721 ---------+---------+---------+---------+---------+---------+ 3780
         TCGAAAAGGAGTGGTCCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT

a        S  F  S  S  P  G  A  R  L  P  L  P  T  *  E  *  S  I  P  R  -
b         A  F  P  H  Q  E  P  G  F  H  S  P  H  R  N  S  P  S  P  D  -
c          L  F  L  T  R  S  P  A  S  T  P  H  I  G  I  V  H  P  Q  I -

         TTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTG
    3781 ---------+---------+---------+---------+---------+---------+ 3840
         AAGCGGTAACAAGTGGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC

a        F  A  I  V  H  P  S  P  C  P  P  L  P  S  T  P  T  I  Q  V  -
b         S  P  L  F  T  P  R  P  A  L  L  C  L  P  P  P  P  S  R  W  -
c          R  H  C  S  P  L  A  L  P  S  F  A  F  H  P  H  H  P  G  G -

         GAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
    3841 ---------+---------+---------+---------+---------+---------+ 3900
         CTCTGGGACTCTTCCTGGGACCCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC
```

FIG. 51
(CONTINUED)

```
a        E  T  L  R  R  T  L  G  A  L  G  I  W  S  D  Q  R  C  A  L  -
b         R  P  *  E  G  P  W  E  L  W  E  F  G  V  T  K  G  V  P  C  -
c          D  P  E  K  D  P  G  S  S  G  N  L  E  *  P  K  V  C  P  V -

         TACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
    3901 ---------+---------+---------+---------+---------+---------+ 3960
         ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA

a        Y  T  G  E  D  P  A  P  G  W  G  S  L  W  V  K  L  G  G  G  -
b         T  Q  A  R  T  L  H  L  D  G  G  P  C  G  S  N  W  G  E  V  -
c          H  R  R  G  P  C  T  W  M  G  V  P  V  G  Q  I  G  G  R  C -

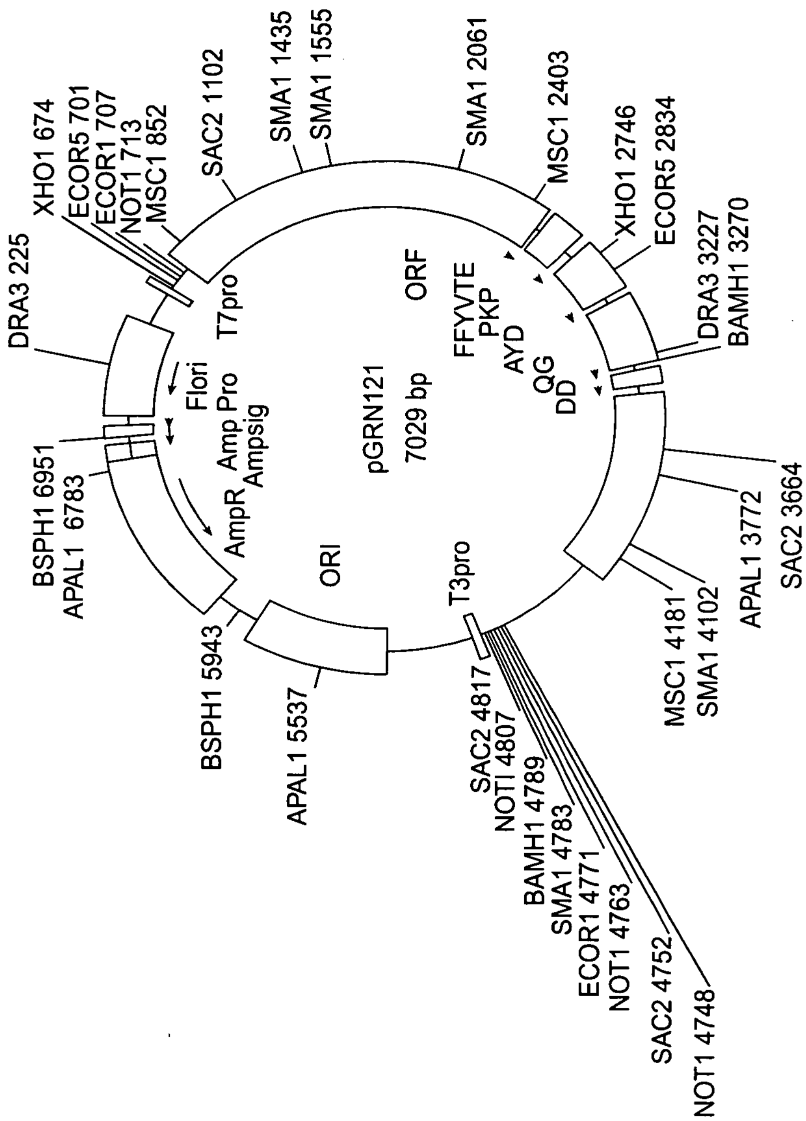
         GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAA
    3961 ---------+---------+---------+---------+---------+---------+ 4020
         CGACACCCTCATTTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTTT

a        A  V  G  V  K  Y  *  I  Y  E  F  F  S  F  E  K  K  K  K  K  -
b         L  W  E  *  N  T  E  Y  M  S  F  S  V  L  K  K  K  K  K  K  -
c          C  G  S  K  I  L  N  I  *  V  F  Q  F  *  K  K  K  K  K  K -

         AAAAAAAAA
    4021 --------- 4029
         TTTTTTTTT

a        K  K  K   -
b         K  K     -
c          K  K    -
```

FIG. 51
(CONTINUED)



DRA3 225
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
SAC2 1102
SMA1 1435
SMA1 1555
SMA1 2061
MSC1 2403
XHO1 2746
ECOR5 2834
DRA3 3227
BAMH1 3270
SAC2 3664
APAL1 3772
SMA1 4102
MSC1 4181
SAC2 4817
NOTI 4807
BAMH1 4789
SMA1 4783
ECOR1 4771
NOT1 4763
SAC2 4752
NOT1 4748
APAL1 5537
BSPH1 5943
APAL1 6783
BSPH1 6951
T7pro
T3pro
ORF
FFYVTE
PKP
AYD
QG
DD
Flori
Amp Pro
Ampsig
AmpR
ORI
pGRN121
7029 bp

FIG. 52

```
                                                                1
                                                              met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

                                     10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

                 20                                      30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                     40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

                 50                                      60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                     70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

                 80                                      90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                    100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

                110                                     120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

                                    130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

                140                                     150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                    160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

                170                                     180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                    190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT
```

FIG. 53

```
          200                                         210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

            230                                     240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

            260                                     270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
            290                                     300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

            320                                     330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

                                340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

            350                                     360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

                                370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

            380                                     390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

                                400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

            410                                     420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA
```

FIG. 53
(CONTINUED)

```
                                        430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

            440                                         450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

            470                                         480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

            500                                         510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

            530                                         540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

                                550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

            560                                         570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                                580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

            590                                         600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG
                                610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

            620                                         630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

                                640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC
```

FIG. 53

(CONTINUED)

```
            650                                     660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

                                670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

            680                                     690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

                                700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

            710                                     720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

                                730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

            740                                     750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

                                760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

            770                                     780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

                                790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

            800                                     810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

                                820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

            830                                     840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

                                850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

            860                                     870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG
```

FIG. 53
(CONTINUED)

```
                                      880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

            890                                         900
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

                                      910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

            920                                         930
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC
                                      940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

            950                                         960
ser ser tyr ala arg thr ser ile arg ala ser leu thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC

                                      970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

            980                                         990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

                                      1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

            1010                                        1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

                                      1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

            1040                                        1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

                                      1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

            1070                                        1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

                                      1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC
```

FIG. 53
(CONTINUED)

```
              1100                                      1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

                                  1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

              1130      1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA
```

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCC

AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC

GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC

CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG

CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT

CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA

GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA

CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC

TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAA

AAAAAAAAAA

FIG. 53
(CONTINUED)

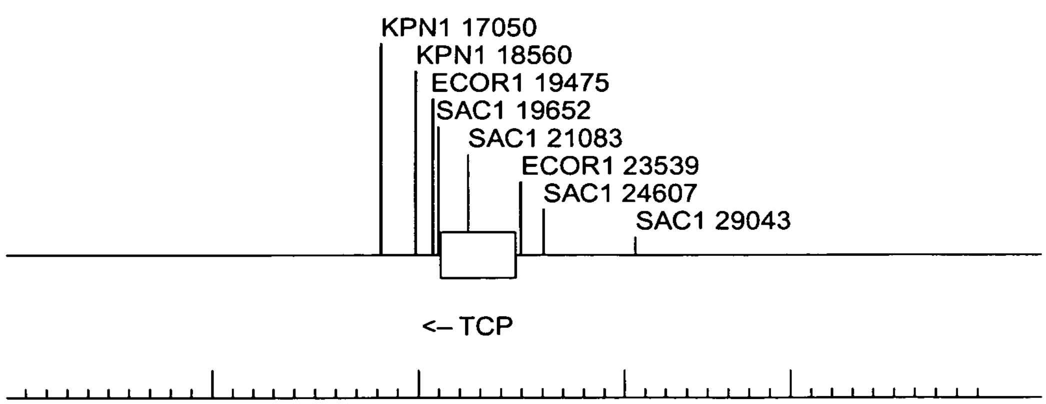


FIG. 54